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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB
Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                       Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq length: seq length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268485 seqs, 34193795 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapop 60.0 , Gapext 60.0
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                                                                                                                                       Length
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                                                                                                                                                                      SUMMARIES
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85.089 Million cell updates/sec
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	P70491	W29319	W29318	W29317	W29316	W29315	R56485	W29320	Y84022	Y84021	W59218	W59217	W29314	W29313	W29311	W29312	Y80517	Y80516	W04209	W04210	W04208	Y28928	W29308	W04211	R34722	Y44700	W29310	W29309	R56484	Y84020	P70492	P80160	Y80514
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		Streptavidin prote				prot		tavidi	acid	98	strep	. avidinii strep	treptavidin					Streptomyces avidi	Mutant streptavidi	Mutant Streptomyce	-	•	Recombinant Core-s		Core streptavidin.	-		prot	pRAS109	ω		osynthetic prote	Streptomyces avidi

## ALIGNMENTS

PESULT P60625
ID P6
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AC P6
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XX P7
XX P DNA sequences and hybrid DNA sequences - encoding streptavidin-like polypeptide, also joined to another protein, e.g. tissue plasminogen activator Disclosure; Fig. 2; 54pp; English WPI; 1986-106643/16. N-PSDB; N60626. Meade HM, WO8602077-A Streptomyces. Antibiotic; biotin binding affinity; fusion protein Sequence of a streptavidin-like polypeptide encoded by SA307 13-AUG-1991 P60625; 02-OCT-1984; 01-OCT-1985; 10-APR-1986 P60625 standard; Protein; 183 AA. (MEAD/) MEADE H M. Garwin JL, (first entry) 84US-0656873. 85WO-0001901 Biogen ¥

The inventors claim the DNA sequence in SA307 which codes for a

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RESULT
P93530
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                       : 04 -JUN-1990
Streptavidin is a 60kD protein isolated from Streptomyces avidinii that binds extremely tightly to the vitamin biotin. It is composed of four
                                                           DNA sequence encoding streptavidin and vector - comprising hybrid gene encoding fusion protein with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                steptavidin-like polypeptide (see N60626), and the polypeptide encoded by it (P60625). They also claim hybrid Sos comprising N60626 and a second sequence coding for another protein, polypeptide, peptide or AA (pref. tissue plasminogen activator (TPA)).
                             Fig 1; page 1/5;
                                                 biotin-binding activity
                                                                                                                                                                                                                                                                                                                                                  Streptavidin protein.
                                                                                          WPI; 1989-130040/17.
                                                                                                              Edwards
                                                                                                                                  (BRBI-) BRIT
                                                                                                                                                      08-OCT-1987;
                                                                                                                                                                           07-OCT-1988;
                                                                                                                                                                                                                  W08903422-A
                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                          Streptomyces
                                                                                                                                                                                                                                                                                                                              Streptavidin;
                                                                                                                                                                                                                                                                                                                                                                                           P93530;
                                                                                                                                                                                                                                                                                                                                                                                                              P93530 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vqq 183
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                                                                                                               RM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                           avidinii.
                                                                                                                                  BIO-TECHN LTD
                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                              Streptomyces avidinii; biotin
                                                                                                                                                      87GB-0023661
                                                                                                                                                                          88WO-GB00831.
                                                                                                                                                                                                                                                        /note="Leader sequence"
25..159
                                                                                                                                                                                                                                   /note="This sequence was as the basis for the design
for the synthetic gene of the present invention."
                                                                                                                                                                                                                                                                                     Location/Qualifiers
                             22pp; English
                                                                                                                                                                                                                                                                                                                                                                                                             protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                               183
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Pred. No. 7.6e-173;
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Streptavidin prodn. from Bacillus subtilis - using signal p from bacterial exo-protein and expression element from Gram
                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               identical subunits of 15kD and binds 4 mole of biotin per mole of protein. It is structurally related to the protein avidin. It can be readily conjugated to a range of other proteins. In order to facilitate the incorporated of streptavidin into expression vectors and the production of novel chimeric proteins containing streptavidin has functionality, an improved novel synthetic gene for streptavidin has been constructed (n90755) based on the amino acid sequence of mature
                                   P-PSDB;
                                                                  Nagarajan V;
                                                                                                             29-MAY-1992;
                                                                                                                                     27-MAY-1993;
                                                                                                                                                           09-DEC-1993
                                                                                                                                                                                 W09324631-A
                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                         Streptomyces
                                                                                                                                                                                                                                                                                                                             Streptavidin; protein secretion;
                                                                                                                                                                                                                                                                                                                                                    Streptavidin
                                                                                                                                                                                                                                                                                                                                                                          27-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                R44491;
                                                                                                                                                                                                                                                                                                                                                                                                                       R44491 standard; Protein; 183 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      streptavidin.
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                                 1993-405822/50.
DB; Q53412.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                   gene.
                                                                                                                                                                                                                                                                                                         avidinii.
                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                               92US-0891524
                                                                                                                                     93WO-US05240
                                                                                                                                                                                                                  /label= streptavidin 37..183
                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                       25..183
                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                 'label= signal_peptide
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Pred. No. 7.6e-173;
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                                                                                                                                                                                                                                                                                                                               Bacillus subtilis
                                                                                                                                                                                                     transformed
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                                                                                                                                                                                                                                                                                               Streptavidin; biotin; anti-interference reagent; detection; mutein; avidin; non-specific binding.
                                                                                                                                                                                                                                                                                                                              Wild-type streptavidin protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tetrameric biologically active streptavidin is produced by secretion from Bacillus subtilis transformed with a plasmid encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 1b; 54pp; English.
Disclosure; Page 17-18; 26pp; German
                             Streptavidin and avidin muteins with reduced binding affinity for biotin - useful for reducing interference from nonspecific binding
                                                             WPI; 1997-482043/45
N-PSDB; T73193.
                                                                                                   Brandstetter H,
                                                                                                                                            01-APR-1996;
                                                                                                                                                                                                      DE19637718-A1
                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                  27-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                       W29306;
                                                                                                                                                                                                                                                                                                                                                                                           W29306 standard; Protein; 183 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             positive bacterial protein
                                                                                           Schmitt U;
                                                                                                                                                               16-SEP-1996;
                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                             Peptide
                     in assays
                                                                                                                       (BOEF ) BOEHRINGER MANNHEIM GMBH.
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1..24
/label= signal
25..183
                                                                                                                                                               96DE-1037718
                                                                                                  Deger A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 183; DB 14; 100.0%; Pred. No. 7.6e-173;
                                                                                                   Engh R,
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                                                                                                  Kopetzki E,
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                                                                                                    Mueller
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a streptavidin which is used in a novel method of reducing interference from non-specific binding in assays. Mutchns constructed from a core streptavidin or avidin sequence are selected that differ from the native polypeptide by at least one amino acid and have a binding affinity for biotin of less than 1010 1/mole. The biotin-bindable polypeptide may be present as a polymeric conjugate, e.g. with another polypeptide or protein, especially bovine serum albumin. These muteins are used as anti-interference reagents for reducing and/or avoiding nonspecific interactions in a process for detecting an analyte. In particular, they are used in assays where the streptavidin/avidin-biotin specific binding pair is involved for qualitative and/or quantitative determination of an analyte in a test sample, e.g. a heterogeneous immunoassay or a hybridisation assay. Despite having a lower binding affinity for biotin, the mutein have high immunological cross-reactivity in the streptavidin and acid in the second of the content of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W59216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptavidin; purification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
Streptavidin mutants with higher binding affinity for peptide ligands - have mutation in amino acid region 44-53, used to 1
                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                avidinii streptavidin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W59216 standard; Protein; 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                with native streptavidin and avidin
                                                                         N-PSDB; V34714.
                                                                                             WPI; 1998-218868/20
                                                                                                                                            Skerra A,
                                                                                                                                                                                                                                       10-OCT-1996;
                                                                                                                                                                                                                                                                                     09-OCT-1997;
                                                                                                                                                                                                                                                                                                                                    15-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                EP835934-A2
                                                                                                                                                                                        (BIOA-) INST BIOANALYTIK GMBH GOETTINGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 VQQ 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 VGGAEARINTQWLLTSGTTEANAWKSTLVGHDTETKVKPSAASIDAAKKAGVNNGNPLDA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vqq 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vggaearintqwlltsgtteanawkstlvghdtftkvkpsaasidaakkagvnngnplda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      galtgtyesavgnaesryvltgrydsapatdgsgtalgwtvawknnyrnahsattwsgqy
                                                                                                                                            Voss S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                             avidinii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ligand; binding affinity; mutant; isolation; recover; immobilise.
                                                                                                                                                                                                                                       96DE-1041876.
                                                                                                                                                                                                                                                                                     97EP-0117504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                      Avidin;
hybrid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence encodes a wild-type streptavidin protein isolated from Streptomyces avidini. This sequence is used to produce mutants which are used in a method to assay the binding affinity of streptavidin mutants. These mutants have a mutation within the amino acid (aa) region 44-53 of the wild-type protein show a higher binding affinity than the wild-type for peptide ligands that include the sequence of formula Trp-X-His-pro-Gln-Phe-Y-Z where X = any aa; Y and Z are both Gly, or Y = Glu and Z = Arg or Lys. Recombinant streptavidin mutants can be used to isolate, purify and determine proteins or to determine/recover substances that contain streptavidin-binding groups. Such compounds may also be used to immobilise fusions on microtitre plates, microbeads or
        WPI; 1999-385599/32.
N-PSDB; X80198.
                                                     Cederholm-Williams SA;
                                                                                                             09-DEC-1997;
                                                                                                                                       09-DEC-1998;
                                                                                                                                                                                                W09929838-A1
                                                                                                                                                                                                                            Streptococcus
                                                                                                                                                                                                                                                                                                 Streptococcus streptavidin.
                                                                                                                                                                                                                                                                                                                          20-AUG-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                         Y17868;
                                                                                                                                                                                                                                                                                                                                                                                    Y17868 standard; Protein; 183 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sensor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page -; 21pp; German.
                                                                               (BRIM ) BRISTOL-MYERS SQUIBB CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   make the mutant streptavidin proteins represented in W59217 and W59218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           purify or determine fusion proteins including these ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MRKIVVAAIAVSLTTVSITASASADPSKDSKAQVSAAEAGITGTWYNQLGSTFIVTAGAD 60
                                                                                                                                                                                                                                                                                                                                                                                                                σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VQQ 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GALTGTYESAVGNAESRYVLTGRYDSAPATDGSGTALGWTVAWKNNYRNAHSATTWSGQY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mrkivvaaiavslttvsitasasadpskdskaqvsaaeagitgtwynqlgstfivtagad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence does not appear in the specification but is used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chips
                                                                                                                                                                                                                                                     streptavidin; batroxobin; fibrinogen converting enzyme; fusion protein; sealant; surgery; reduce bleeding; fibr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                             97us-0067978
                                                                                                                                       98WO-US26086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 183; DB 19; 100.0%; Pred. No. 7.6e-173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 183;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cc protein (FCE). The fusion protein is a multidomain protein comprising:

Cc (a) a FCE; and (b) a first member of a binding pair, that is linked to

Ct the FCE chain: (i) directly by bonds utilizing the N-terminal amino

CC groups, the C-terminal carboxy groups or side-chain functionalities;

Cc (ii) via a bifunctional linkage moiety linking the groups or

CC functionalities; or (iii) by the first member binding to the second

CC member of the binding pair, where the second member of the binding pair

CC is covalently attached to the first polypeptide chain. The FCE can be

CC used in a method for producing fibrin. Fibrin is useful as a sealant in

CC surgery to, e.g. reduce bleeding by sealing blood vessels, and tissues

CC that have been dissected either in surgery or through wounding. The

CC fusion protein allows for the removal of the fibrinogen converting

CC enzyme from the fibrin sealant preparation via the binding of

CC streptavidin to a biotin solid support. The present sequence represents

CC Streptococcus streptavidin as given in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                               Potato proteinase inhibitor-II; PPI-II; streptavidin; worm; insect; plant-noxious protein; pest resistance; moth; insect; weevil; grub; beetle; fly; thrip; locust; cricket; borer; mite; looper;
15-JUL-1998;
                                                                          27-JAN-2000.
                                                                                                               W0200004049-A1
                                                                                                                                                                   Peptide
                                                                                                                                                                                         Key
                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                             Streptavidin
                                                                                                                                                                                                                                                                                                                                                                                                  25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                       Y44701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y44701 standard; Protein; 183 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 28; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A fibrinogen-converting enzyme fusion protein
                                     15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 VQQ 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 VGGAEARINTQWLLTSGTTEANAWKSTLVGHDTFTKVKPSAASIDAAKKAGVNNGNPLDA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 vggaearintqwlltsgtteanawkstlvghdtftkvkpsaasidaakkagvnngnplda 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MRKIVVAAIAVSLTTVSITASASADPSKDSKAQVSAAEAGITGTWYNQLGSTFIVTAGAD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present invention describes a fibrinogen-converting enzyme fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vqq 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GALTGTYESAVGNAESRYVLTGRYDSAPATDGSGTALGWTVAWKNNYRNAHSATTWSGQY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  galtgtyesavgnaesryvltgrydsapatdgsgtalgwtvawknnyrnahsattwsgqy 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                           protein for recombinant pART27 vector.
 98NZ-0331002
                                     99WO-NZ00110
                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 183; DB 20; 100.0%; Pred. No. 7.6e-173; tive 0; Mismatches 0;
                                                                                                                                                "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 183;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 183; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is streptavidin, a plant-noxious protein. Recombinant vector, pART27 expressing a chimeric polypeptide comprising streptavidin mature peptide fused to the potato proteinase inhibitor-II (PPI-II) signal peptide is targetted to the vacuole.

Transformation of plant genome with the vector can produce pest resistance in plants, plant derived products and stored harvest material. Pests that can be controlled include, cotton bollworm, tropical army-worm, European corn-borer or red mite, tobacco horn worm, loopers, rice stem borer, porina, cutworms, diamondback moth, potato tuber moth, codling moth, Indian meal moth, gypsy moth, argentine stem weevil, clover root weevil, grass-grubs, corn rootworm, rice and wheat weevils, mealworms, flour beetles, black field cricket, locusts, sawflies, Western flower thrips, Hessian flies or two-spotted mite.
                                                                                                                          Plant somatic tissue degeneration; plant essential factor; deplet viability; sps gene; plant development; plant morphology; flower;
30-JUL-1999;
                                                                                  Streptomyces avidinii.
                                                                                                                                                                         Streptomyces
                                                                                                                                                                                                     06-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 12; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-171244/15
N-PSDB; Z49867.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Christeller JT,
                            17-FEB-2000
                                                       WO200007427-A2
                                                                                                                                                                                                                                                           Y80512 standard; Protein; 186 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HORT-) HORTICULTURE & FOOD
                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                            181 VQQ 183
                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chimeric polypeptide and composition comprising the ful for conferring pest resistance on plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GALTGTYESAVGNAESRYVLTGRYDSAPATDGSGTALGWTVAWKNNYRNAHSATTWSGQY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                               galtgtyesavgnaesryvltgrydsapatdgsgtalgwtvawknnyrnahsattwsggy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mrkivvaalavslttvsitasasadpskdskaqvsaaeagitgtwynqlgstfivtagad
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                                                                                                                                                                                                                                                                                                                                  vqq 183
                                                                                                                plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
ilarity 100.0%;
Conservative (
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                                                                                                                                                                      avidinii sps
                                                                                                                                                                                                    (first entry)
99WO-IL00420.
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                                                                                                                                                                      protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 183; DB 21;
Pred. No. 7.6e-173;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INST NEW ZEALAND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Markwick NP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide
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                                                                                                                                            depletion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method of effecting degeneration of a somatic plant tissue by expressing a heterologous protein capable of binding a plant essential factor (PEP), in somatic plant tissue cells, where heterologous protein expression causes depletion of the PEF so the plant viability is maintained, while simultaneous degeneration of the somatic plant tissue is effected. This sequence represents the Streptomyces avidinii sps protein as an example of a heterologous protein introduced into the plants. The methods can provide for the selective and optionally reversible cell degeneration in somatic plant tissue. They can be used to example controlling plant development and morphology. They can be used e.g. to decrease the number of flowers in fruit producing plants
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                                                      Streptomyces avidinii
                                                                                               Plant somatic tissue degeneration; plant essential factor; viability; mst gene; plant development; plant morphology; f
                                                                                                                                           Streptomyces avidinii mst protein.
                                                                                                                                                                        06-JUN-2000
                                                                                                                                                                                                      Y80513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                           WO200007427-A2
                                                                                                                                                                                                                                  Y80513 standard; Protein; 184 AA
                                                                                   fruit plant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GALTGTYESAVGNAESRYVLTGRYDSAPATDGSGTALGWTVAWKNNYRNAHSATTWSGQY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MRKIVVAAIAVSLTTVSITASASADPSKDSKAQVSAAEAGITGTWYNQLGSTFIVTAGAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mrkivvaalavslttvsitasasadpskdskaqvsaaeagitgtwynqlgstf1vtagad
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                                                                                                                                                                                                                                                                                                                                                                                                                        galtgtyesavgnaesryvltgrydsapatdgsgtalgwtvawknnyrnahsattwsgqy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 AA;
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ilarity 100.0%;
Conservative (
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                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98IL-0125632.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            number of fruits which reach maturity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 183; DB 21; Pred. No. 7.7e-173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 186;
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RESULT 10
Y80515
ID Y80515
XX Y80515
XX O6-JUN
DT 06-JUN
DT 05-JUN
CXX Strept
XX Plant
KW Viabil
KW Fruit
XX Fruit
XX Strept
XX Strept
XX W02000
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Best Local
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                                   Streptomyces avidinii
                                                                                 Plant somatic tissue degeneration; plant essential factor; depletion; viability; mprost gene; plant development; plant morphology; flower;
                                                                                                                                     Streptomyces avidinii mprost protein.
                                                                                                                                                                       06-JUN-2000 (first entry)
 WO200007427-A2
                                                                                                                                                                                                                                          Y80515 standard; Protein; 161 AA.
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                                                                  fruit plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method of effecting degeneration of a somatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Examples; Page 85; 91pp; English.
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184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RKIVVAAIAVSLTTVSITASASADPSKDSKAQVSAAEAGITGTWYNQLGSTFIVTAGADG
                                                                                                                                                                                                                                                                                                                                                                                          ggaearintqwlltsgtteanawkstlvghdtftkvkpsaasidaakkagvnngnpldav 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                             altgtyesavgnaesryvltgrydsapatdgsgtalgwtvawknnyrnahsattwsgqyv 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rkivvaaiavslttvsitasasadpskdskaqvsaaeagitgtwynqlgstfivtagadg 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182;
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RESULT
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ID R56483
XX R56
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XX R56
XX R56
XX R56
XX SGF
XX SGF
XX SGF
XX MMP
XX W09
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plant tissue by expressing a heterologous protein capable of binding a plant essential factor (PEF), in somatic plant tissue cells, where heterologous protein expression causes depletion of the PEF so the plant viability is maintained, while simultaneous degeneration of the somatic
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                                               WO9415644-A.
                                                                                                              Amplification; single chain variable region fusion protein; PCR.
                                                                                                                                               ScFV pRAS108
                                                                                                                                                                               26-MAR-1995
                                                                                                                                                                                                                                                R56483 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reach maturity.
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                                                                                                                                                                                                                                                                                                                                             144 WKSTLVGHDTFTKVKPSAASIDAAKKAGVNNGNPLDAVQQ 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          adpskdskaqvsaaeagitgtwynqlgstfivtagadgaltgtyesavgnaesryvltgr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADPSKDSKAQVSAAEAGITGTWYNQLGSTFIVTAGADGALTGTYESAVGNAESRYVLTGR 83
                                                                                                                                                                                                                                                                                                                              wkstlvghdtftkvkpsaasidaakkagvnngnpldavqq
                                                                                                                                                                                                                                                                                                                                                                                          ydsapatdgsgtalgwtvawknnyrnahsattwsgqyvggaearintqwlltsgtteana 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.4%; Score 160; DB 21; ilarity 100.0%; Pred. No. 3.2e-150; Conservative 0; Mismatches 0;
                                                                                                                                             and pRAS112
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                                                                                                                                                                             (first entry)
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by expressing a heterologous protein capable of binding a
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                                                                                                                                                                                                                                                Protein;
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21-JUL-1994

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RESULT 12
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Best Local :
                  DNA sequence encoding streptavidin and vector - comprising hybrid gene encoding fusion protein blotin-binding activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biotin; chimeric gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mature streptavidin as encoded by a synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New cpds. comprising a targetting portion and a cytotoxic por used esp. for treating mammals for destroying target cells,
                                                                                                                                                                                                                                                                                                                                                      07-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                                     20-APR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO8903422-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptavidin; synthetic gene; Streptomyces avidinii;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-JUN-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 9; 114pp; English.
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                                                                                                                                                                                                                                                  (BRBI-) BRIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 ADPSKDSKAQVSAAEAGITGTWYNQLGSTFIVTAGADGALTGTYESAVGNAESRYVLTGR 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence is that of the ScFv pRAS108 and pRAS112 between HindIII and RI site obtd. by PCR.
                                                                                                                      1989-130040/17.
DB; N90755.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WKSTLVGHDTFTKVKPSAASIDAAKKAGVNNGNPLDAVQQ 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1994-248907/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ydsapatdgsgtalgwtvawknnyrnahsattwsgqyvggaearintqwlltsgtteana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     435 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                  BIO-TECHN LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Epenetos AA,
                                                                                                                                                                                                                                                                                                    87GB-0023661.
                                                                                                                                                                                                                                                                                                                                                      88WO-GB00831.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93GB-0000686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94WO-GB00087.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spooner RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 160; DB 15; I
Pred. No. 8.2e-150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                          protein with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          portion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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RESULT
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 159;
plant tissue by expressing a heterologous protein capable of binding a plant essential factor (PEF), in somatic plant tissue cells, where heterologous protein expression causes depletion of the PEF so the plant viability is maintained, while simultaneous degeneration of the somatic plant tissue is effected. This sequence represents the Streptomyces avidinii prost protein as an example of a heterologous protein introduced into the plants. The methods can provide for the selective and optionally
                                                                                               The
                                                                                                                                                          Degeneration of somatic plant tissue by expression of a heterologous protein, useful for controlling plant development and morphology, such as decreasing the number of flowers present to increase the number of
                                                                                                                                                                                                                             WPI; 2000-195402/17.
                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces avidinii
                                                                                                                                                                                                                                                                                                                                                                                                                                            viability; prost gene;
fruit plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant somatic tissue degeneration; plant essential factor; depletion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces avidinii prost protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The synthetic gene is constructed from 24 oligomers (BB214-BB237) which were synthesised by automated phosphoramidite chemistry. Apart from Met-1, it has the same sequence as natural mature streprotein produced by Streptomyces avidinii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fig
                                                                                                                      Examples; Page
                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                                            03-AUG-1998;
                                                                                                                                                                                                                                                                                                                                     30-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                        WO200007427-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y80514 standard;
                                                                                                                                                                                                                                                                                  (AGRI-) AGRIC RES ORG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13
                                                                                            invention relates to a method of effecting degeneration of a somatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSAPATDGSGTALGWTVAWKNNYRNAHSATTWSGQYVGGAEARINTQWLLTSGTTEANAW 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dsapatdgsgtalgwtvawknnyrnahsattwsgqyvggaearintqwlltsgtteanaw 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                page 2/5; 22pp;
                                                                                                                                                                                                                 Z91075.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.9%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                      Ginzberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                      86; 91pp; English
                                                                                                                                                                                                                                                                                                            98IL-0125632
                                                                                                                                                                                                                                                                                                                                     99WO-IL00420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        plant development; plant morphology; flower;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 159; DB 10; 1
Pred. No. 3.1e-149;
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 introduced optionally
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RESULT 14
P80160
XX Biosyn
XX Biosyn
XX Biosyn
XX W08809
XX W08809
PN W08809
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  Matches
                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local 9
                                                                                                                                                                                                                                               Multi-functional biosynthetic protein comprising single chain BABS and streptavidin protein trailer linked via a spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reversible cell degeneration in somatic plant tissue. They can be used for artificially controlling plant development and morphology. They can be used e.g. to decrease the number of flowers in fruit producing plants so as to increase the number of fruits which reach maturity.
                                                                                                                                                                                                                                                                                                                                                                                 Recombinant multifunctional protein - having an antibody binding site and a sequence for biological activity, ion sequestering or binding to a solid support.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biosynthetic Antibody Binding site (BABS); variable domain; anti-CEA monoclonal antibody; streptavidin.
                                                                                                                                    Sequence
                                                                                                                                                                                              See also N80171-N80192
                                                                                                                                                                                                                                                                                                                                Disclosure; ; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Huston JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-MAY-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO8809344-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-OCT-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CREA-) CREATIVE BIOMOLECULES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1988-353928/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSAPATDGSGTALGWTVAWKNNYRNAHSATTWSGQYYGGAEARINTQWLLTSGTTEANAW 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DPSKDSKAQVSAAEAGITGTWYNQLGSTFIVTAGADGALTGTYESAVGNAESRYVLTGRY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dsapatdgsgtalgwtvawknnyrnahsattwsgqyvggaearintqwlltsgtteanaw
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  159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N80186
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86.9%; Score 159; DB 9; Liarity 100.0%; Pred. No. 3.2e-149; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oppermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein with streptavidin trailer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87US-0052800.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₽
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                                                 Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 162;
Indels
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0;
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Gaps
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                                                                                                     Query Match
Best Local
                                                                                         Matches
                                                                                                                                                                                The sequence is that of streptavidin from S.avidinii. Streptavidin may be expressed from a fusion gene comprising its coding gene and encoding a target protein of interes, where he streptavidin has binding sites for biotin or deriv. The streptavidin has 4 binding sites free for biotin, and is produced free of biotin contamination. Improved streptavidins may also be produced by site-directed mutagenesis. The fused gene may be used to produce labelled, chemically modified proteins in vivo, and to isolate
                                                                                                                                                                                                                                                                                                                                                                                                         (UYNY-)
                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                         Disclosure; Figure 3;
                                                                                                                                                                                                                                                                                                               DNA encoding streptavidin - obtd. by restriction endo-nuclease digestion of chromosomal DNA of Streptomyces avidinii
                                                                                                                                                                                                                                                                                                                                                            WPI; 1987-250198/35
                                                                                                                                                                                                                                                                                                                                                                                   Cantor CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO8705026-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptavidin; N-terminal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptavidin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P70492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P70492 standard;
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 91
                                             μ
                                                                                                      Local Similarity
                      92 GSGTALGWTVAWKNNYRNAHSATTWSGQYVGGAEARINTQWLLTSGTTEANAWKSTLVGH 151
                                                                   32 AQVSAAEAGITGTWYNQLGSTFIVTAGADGALTGTYESAVGNAESRYVLTGRYDSAPATD 91
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KSTLVGHDTFTKVKPSAASIDAAKKAGVNNGNPLDAVQQ
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                                            aqvsaaeagitgtwynqlgstfivtagadgaltgtyesavgnaesryvltgrydsapatd
                                                                                         152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dsapatdgsgtalgwtvawknnyrnahsattwsgqyvggaearintgwlltsgtteanaw 124
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                                                        N70810.
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                                                                                                                                                    182 AA;
                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence
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                                                                                                    83.1%;
                                                                                                                                                                                                                                                                                      54pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fusion gene;
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                                                                                         0; Mismatches
                                                                                                     Score 152; DB 8; L: Pred. No. 2.8e-142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fusion protein;
                                                                                          0;
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Search Job ti	D Oy
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Search completed: April 6, 2001, 01:25:30 Job time: 2004 sec	152 DTFTKVKPSAASIDAAKKAGVNNGNPLDAVQQ 183 
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	183 182

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gb_pat1:A39565
gb_pat1:A93152
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Query: US-09-589-870-2
Query length: 183
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Database length: -1736092196
Search time (sec): 929.150000
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8.2e-05
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A9383 Sequence 7 from Patent W 109059 Sequence 38 from Patent W 109059 Sequence 38 from Patent W 100743 S.avidinii synthetic gen A00744 S.avidinii synthetic gen A00744 S.avidinii synthetic gen A00744 S.avidinii synthetic gen A00744 S.avidinii synthetic gen India Sequence 2 from Patent U 101349 Sequence 2 from Patent U 101349 Sequence 6 from Patent W 101349 Sequence 6 from Patent I A79145 Sequence 6 from Patent I X65082 Synthetic gene for street I X65082 Synthetic gene for street I X14583 Artificial sequence; I Y14583 Artificial sequence I From Patent I I17472 Sequence 15 from Patent I I17472 Sequence 8 from Patent I A193563 Sequence 8 from Patent I A79156 Sequence 8 from Patent I A79156 Sequence 8 from Patent I X78782 Streptavidin v1 [Streptoavi I S78777 streptavidin v2 [Streptoavi I S78777 streptavidin v2 [Streptoavi I S78772 streptavidin v2 [Streptoavi I S78782 streptavidin v2 [Streptoavi I S78782 streptavidin v2 [Streptoavi I 149879 Sequence 78 from Patent U 14980 Sequence 79 from Patent I 14980 Sequence I from Patent I 14980 Sequence I from Patent I 1493653 Sequence I from Patent I 1493657 Sequence I from Patent I I 1493657 Sequence I I from Patent I I 1493657 
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A93649 Sequence 1 from Patent I
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A93152 Sequence 4 from Patent
AR082490 Sequence 4 from paten
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gb_pat1:A93660
gb_ba2:ECPROTG
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SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
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Align seg 1/1 to: SASTRAVG
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                                                                                                                                                                                                                       1 MetArgLysIleValValAlaAlaIleAlaValSerLeuThrThrValSe
                                                                                                                                                       rIleThrAlaSerAlaSerAlaAspProSerLysAspSerLysAlaGlnV
alSerAlaAlaGluAlaGlyIleThrGlyThrTrpTyrAsnGlnLeuGly
                                                                  TCTCGGCCGCAGGCCGGCATCACCGGCACCTGGTACAACCAGCTCGGC
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Streptomyces avidinii.
Streptomyces avidinii
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Streptomyces
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Streptomyces avidinii gene
X03591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Argarana, C.E., Kuntz, I.D., Birken, S., Axel, R. and Cantor, C.R. Molecular cloning and nucleotide sequence of the streptavidin gene Nucleic Acids Res. 14 (4), 1871-1882 (1986)
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/db_xref="GI:46741"
/db_xref="SGI:56-PROT:P22629"
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WKNNYRNAHSATTWSGQYVGGAEARINTQWLLTSGTTEANAWKSTLVGHDTFTKVKPS
AASIDAAKKAGVNNGNPLDAVQQ"
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/db_xref="taxon:1895"
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0 i A93660 Sequence 12 from Paten
200 i X71365 E.chrysathus gene
319 i Y18681 Gallus gallus genomi
0128 i AE005021 Halobacterium sp.
0166 i AE000094 Rhizobium sp. NGR
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                                                                          Quality:
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Mueller,R.D. and Deger,A.D.
Recombinant inactive core streptavidin mutants
Patent: EP 0799890-A 08-OCT-1997;
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                                                                                                                                                 Patent: WO 9415644-A 4 21-JUL-1994;
IMP CANCER RES TECH (GB)
Other publication GB 2289679 951129
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Epenetos, A.A., Spooner, R.A. and Deonarain,
COMPOUNDS FOR TARGETING
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Epenetos, A.A. and De
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                                                                          TTAAGCCTTCTGCTAGCATTGATGCTGCCAAGAAAGCAGGCGTAAAC
                                                                                                                                                                      ualaAsnAlaTrpLysSerThrLeuValGlyHisAspThrPheThrLysV 157
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AACGGTAACCCTCTAGACGCTGTTCAGCAA 1344
                                    AsnGlyAsnProLeuAspAlaValGlnGln 183
                                                                                                              alLysProSerAlaAlaSerIleAspAlaAlaLysLysAlaGlyValAsn 173
                                                                                                                                                                                                                                  GCTGAGGCTCGTATCAACACTCAGTGGCTGTTAACATCCGGCACTACCGA
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/db_xref="G1:6741541"
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RYDsapatdgsgtalgwtyawknnyrnahsattwsgoyvggaerintqwilltsgtte
aaawkstlvghdfftkykpsaasidaakkagvnngnpldavqq"
a 361 g 306 t
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/db_xref="taxon:32644"
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/codon_start=1
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                                                                  alLysProSerAlaAlaSerIleAspAlaAlaLysLysAlaGlyValAsn 173
                                                                                                                                                                                  ATCGTAATGCGCACAGCGCCACTACGTGGTCTGGCCAATACGTTGGCGGT
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Compounds for targeting
Patent: US 5973116-A 4 26-OCT-1999;
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AR082490
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                              GlyAsnProLeuAspAlaValGlnGln 183
                                                                                                                                                         aAsnAlaTrpLysSerThrLeuValGlyHisAspThrPheThrLysValL 158
                                                                                                                                                                                                                 GluAlaArgIleAsnThrGlnTrpLeuLeuThrSerGlyThrThrGluAl 141
                                                                                                                                                                                                                                                                                                                                                                                                     GluSerArgTyrValLeuThrGlyArgTyrAspSerAlaProAlaThrAs
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                   GGTAACCCTCTAGACGCTGTTCAGCAA 489
                                                                              AGCCTTCTGCTGCCAGCATTGATGCTGCCAAGAAAGCAGGCGTAAACAAC
                                                                                            ysProSerAlaAlaSerIleAspAlaAlaLysLysAlaGlyValAsnAsn 174
                                                                                                                                         GAATGCATGGAAATCGACACTAGTAGGTCATGACACCTTTACCAAAGTTA 412
                                                                                                                                                                                                   GAGGCTCGTATCAACACTCAGTGGCTGTTAACATCCGGCACTACCGAAGC 362
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TARGETED MULTIFUNCTIONAL PROTEINS
Patent: WO 8809344-A 38 01-DEC-1988;
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137 c 133 g
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US-09-589-870-2 x A00743
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LOCUS A00743
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Ratio: 1.000
Percent Similarity: 100.000
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TITLE
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pGlySerGlyThrAlaLeuGlyTrpThrValAlaTrpLysAsnAsnTyrA 108
                                                                                                                                                                                                     GluSerArgTyrValLeuThrGlyArgTyrAspSerAlaProAlaThrAs
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                                                                           rgAsnAlaHisSerAlaThrThrTrpSerGlyGlnTyrValGlyGlyAla 124
                                                              GTAATGCGCACAGCGCCACTACGTGGTCTGGCCCAATACGTTGGCGGTGCT
                                                                                                                         TGGCTCTGGTACCGCTCTGGGCTGGACTGTGGCTTGGAAAAAACAACTATC
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Streptomyces avidinii
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; St
1 (bases 1 to 507)
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S.avidinii synthetic gene for streptavidin.
A00743
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British Bio-Technology Ltd
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SYNTHETIC GENE
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/db_xref="taxon:1895"
10. .492
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ARINTQWLLTSGTTEANAWKSTLVGHDTFTKVKPSAASIDAAKKAGVNNGNPLDAVQQ
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/db_xref="GI:14606"
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/transl_table=11
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LOCUS A00744
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Percent Similarity: 100.000
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                                                                                                                                                             GluSerArgTyrValLeuThrGlyArgTyrAspSerAlaProAlaThrAs
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           rgAsnAlaHisSerAlaThrThrTrpSerGlyGlnTyrValGlyGlyAla
                                                                 pGlySerGlyThrAlaLeuGlyTrpThrValAlaTrpLysAsnAsnTyrA 108
                                                     TGGCTCTGGTACCGCTCTGGGCTGGACTGTGGCTTGGAAAAACAACTATC
GTAATGCGCACAGCGCCACTACGTGGTCTGGCCAATACGTTGGCGGTGCT
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 507)
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British Bio-Technology Ltd
#A00744 is the reverse complement of #A00743.
Location/Qualifiers
1.507
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SYNTHETIC GENE
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/db_xref="taxon:1895"
130 c 137 g 125 t
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                                          TGGCTCTGGTACCGCTCTGGGCTGGACTGTGGCTTGGAAAAAACAACTATC
                                                      pGlySerGlyThrAlaLeuGlyTrpThrValAlaTrpLysAsnAsnTyrA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   synthetic construct
synthetic construct
artificial sequence.
1 (bases 1 to 525)
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KEYWORDS
SOURCE
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FEATURES
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AUTHORS
TITLE
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US-09-589-870-2 x I15647
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LOCUS I15647
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Ratio: 1.000
Percent Similarity: 100.000
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GluSerArgTyrValLeuThrGlyArgTyrAspSerAlaProAlaThrAs 91
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                                                         TGGCTCTGGTACCGCTCTGGGCTGGACTGTGGCTTGGAAAAACAACTATC
                                                                     pGlySerGlyThrAlaLeuGlyTrpThrValAlaTrpLysAsnAsnTyrA 108
                                                                                                              GAATCCCGCTACGTACTGACTGGCCGTTATGACTCTGCACCTGCCACCGA
                                                                                                                                                                        GTGCGGACGGAGCTCTGACTGGCACCTACGAATCTGCGGTTGGTAACGCA 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l (bases 1 to 525)
Lubitz,W. and Szostak,M.P.
Immunogens comprising the non-lytic membrane spanning domain bacteriophages MS2 or Phix174
Patent: US 5470573-A 2 28-NOV-1995;
Location/Qualifiers
1. 525
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Ratio: 1.000
Percent Similarity: 100.000
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                                                   aAsnAlaTrpLysSerThrLeuValGlyHisAspThrPheThrLysValL 158
              yTrpThrValAlaTrpLysAsnAsnTyrArgAsnAlaHisSerAlaThrT 115
                                                                                                                          lyThrTyrGluSerAlaValGlyAsnAlaGluSerArgTyrValLeuThr
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                                                                                                           GAACCTACGAGTCGGCCGTCGGCAACGCCGAGAGCCGCTACGTCCTGACC
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TTGGACGGTGGCCTGGAAGAATAACTACCGCAACGCCCACTCCGCGACCA
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Sequence 2 from Patent US 4839293.
I01349
I01349.1 GI:270125
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Cantor.C.R., Axel.R. and Argarana.C.
DNA encoding streptavidin, streptavidin produced therefrom, polypeptides which include amino acid sequences present in streptavidin and uses thereof patent: US 4839293 A 2 13-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                          Quality:
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LOCUS A39567
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US-09-589-870-2 x A39567
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Percent Similarity:
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40 yIleThrGlyThrTrpTyrAsnGlnLeuGlySerThrPheIleValThrA
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                                                                           unclassified.

1 (bases 1 to 1296)
1 (bases 1 to 1296)
2 (bases 2 to 1290)
2 (compounds FOR TARGETING COMPOUNDS FOR TARGETING Patent: WO 9415644-A 6 21-JUL-1994;
2 (patent: WO 941564-A 6 21-JUL-1994;
3 (patent: WO 941564-A 6 21-JUL-1994;
4 (patent: WO 941564-A 6 21-JUL-1994;
5 (patent: WO 941564-A 6 21-JUL-1994;
6 (patent) FOR TARGETING COMPANY COM
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LOCUS A93154
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A93154
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Epenetos, A.A. and Deonarain, M.
Epenetos for targeting
Compounds for targeting
Patent: EP 0815872-A 07-JAN-1998;
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ANAWKSTLVCHDTFTKVKPSAAS"
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DEFINITION
ACCESSION
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ORIGIN
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AUTHORS
TITLE
JOURNAL
FEATURES
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SOURCE
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Epenetos, A. Antoniou, Spooner, R. Anthe
Compounds for targeting
Patent: US 5973116-A 6 26-OCT-1999;
Location/Qualifiers
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Sequence 6 from patent US
AR082491
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342 c 347 g
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Database sequences: 480022
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536165
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US-09-589-870-2 x X80198
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/cgn2_2/gcgdata/geneseq/geneseqn/NA1999.DAT:883488
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/cgn2_2/gcgdata/geneseq/geneseqn/NA1999.DAT:X83487
                               The present invention describes a fibrinogen-converting enzyme fusion protein (FCE). The fusion protein is a multidomain protein comprising: CC (a) a FCE; and (b) a first member of a binding pair, that is linked to the FCE chain: (i) directly by bonds utilizing the N-terminal amino CC groups, the C-terminal carboxy groups or side-chain functionalities; CC (ii) via a bifunctional linkage molety linking the groups or functionalities; or (iii) by the first member binding to the second CC member of the binding pair, where the second member of the binding pair is covalently attached to the first polypeptide chain. The FCE can be CC used in a method for producing fibrin. Fibrin is useful as a sealant in CC surgery to, e.g. reduce bleeding by sealing blood vessels, and tissues that have been dissected either in surgery or through wounding. The CC fusion protein allows for the removal of the fibrinogen converting CC enzyme from the fibrin sealant preparation via the binding of CC streptavidin to a biotin solid support. The present sequence encodes CC Streptococcus streptavidin as given in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_2/gcgdata/geneseq/geneseqn/NA2000.DAT:z52309
                                                                                                                                                                                                                                                                                                                                                                 A fibrinogen-converting enzyme fusion protein
                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 27-28; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus streptavidin encoding cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             streptavidin; batroxobin; fibrinogen converting enzyme; fusion protein; sealant; surgery; reduce bleeding; fibrin; ss.
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17

from:

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Quality: Ratio:

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167 G;

70

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100.000 183.00

Percent Identity: 100.000

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                                                                                                                                                                                     Streptomyces avidinii sps gene
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2000-195402/17
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                                                                           99WO-IL00420
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                                                                                                                                                          eration; plant essential factor;
development; plant morphology;
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plant tissue by expressing a heterologous protein capable of binding a plant essential factor (PEF), in somatic plant tissue cells, where heterologous protein expression causes depletion of the PEF so the plant viability is maintained, while simultaneous degeneration of the somatic plant tissue is effected. This sequence represents the Streptomyces avidinii sps gene as an example of the heterologous gene introduced into the plants. The methods can provide for the selective and optionally reversible cell degeneration in somatic plant tissue. They can be used for artificially controlling plant development and morphology. They can be used e.g. to decrease the number of flowers in fruit producing plants so as to increase the number of fruits which reach maturity.
                                                                                                                                                                                                                                                                                                       The
                                                                                                                                                                                                                                                                                                                                                                                                                    Degeneration of somatic plant tissue by expression of a heterologous protein, useful for controlling plant development and morphology, such as decreasing the number of flowers present to increase the number of
  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; Y80512.
                                                                                                                                                                                                                                                                                                                                                        Examples;
                                                                                                                                                                                                                                                                                                       invention relates to a method of effecting degeneration of a somatic
    563
                                                                                                                                                                                                                                                                                                                                                   Page 84; 91pp; English.
BP; 107
Α,
    213
C; 169 G;
  74
T; 0 other;
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alignment_block:
US-09-589-870-2 x Z91073
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    Quality:
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Ratio: 1.000
Percent Similarity: 100.000
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HisAspThrPheThrLysValLysProSerAlaAlaSerIleAspAlaAl
                                         ValAlaTrpLysAsnAsnTyrArgAsnAlaHisSerAlaThrThrTrpSe
                                                                                                                                                                                                                         yrAspSerAlaProAlaThrAspGlySerGlyThrAlaLeuGlyTrpThr
                                                                                                                                                                                                                                                                                                                                                                                                                                rGlyGlnTyrValGlyGlyAlaGluAlaArgIleAsnThrGlnTrpLeuL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGCGCAAGATCGTCGTTGCAGCCATCGCCGTTTCCCTGACCACGGTCTC
                                                                                                                                                                                                                                                                               rGluSerAlaValGlyAsnAlaGluSerArgTyrValLeuThrGlyArgT
                                                                                                                                                                                                                                                                                                                      TCGACCTTCATCGTGACCGCGGGGGCGCCGACGGCGCCCTGACCGGAACCTA
                                                                                                                                                                                                                                                                                                                                    SerThrPheIleValThrAlaGlyAlaAspGlyAlaLeuThrGlyThrTy
                                                                                                 CGGCCAGTACGTCGGCGGCGCCGAGGCGAGGATCAACACCCAGTGGCTGC
                                                                                                                                                       GTGGCCTGGAAGAATAACTACCGCAACGCCCACTCCGCGACCACGTGGAG
                                                                                                                                                                                                            ACGACAGCGCCCCGGCCACCGACGGCAGCGGCACCGCCCTCGGTTGGACG
                                                                                                                                                                                                                                                                 CGAGTCGGCCGTCGGCAACGCCGAGAGCCGCTACGTCCTGACCGGTCGTT
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Gaps: 0
Percent Identity: 100.000
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Seq_documentation_block:
ID T73193 standard; DNA; 638 BP.
XX
AC T73193;
XX
DT 27-APR-1998 (first entry)
XX
DE Wild-type streptavidin DNA.
XX
Streptavidin; biotin; anti-inte
KW avidin; non-specific binding; s
OS Unidentified.
XX
                                                                       This DNA sequence encodes a streptavidin which is used in a novel method CC of reducing interference from non-specific binding in assays. Muteins CC constructed from a core streptavidin or avidin sequence are selected that CC differ from the native polypeptide by at least one amino acid and have a binding affinity for blotin of less than 1010 1/mole. The biotin-bindable CC polypeptide may be present as a polymeric conjugate, e.g. with another CC polypeptide or protein, especially bowlne serum albumin. These muteins CC are used as anti-interference reagents for reducing and/or avoiding CC nonspecific interactions in a process for detecting an analyte. In CC particular, they are used in assays where the streptavidin/avidin-biotin CC specific binding pair is involved for qualitative and/or quantitative CC immunoassay or a hybridisation assay. Despite having a lower binding CC affinity for biotin, the muteins have high immunological cross-reactivity core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1997.DAT:T73193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptavidin; biotin; anti-interference reagent; detection; mutein; avidin; non-specific binding; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 16-17; 26pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptavidin and avidin muteins with reduced binding affinity for biotin - useful for reducing interference from nonspecific binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BOEF ) BOEHRINGER MANNHEIM GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       460 CACGACACCTTCACCAAGGTGAAGCCGTCCGCCGCCTCCATCGACGCGGC 509
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244 C;

193 G;

86

T; 0 other;

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Sequence of the sequence of th
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Ratio: 1.000
Percent Similarity: 100.000
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V34714 standard; DN
                                   CDS
                                                                                                                                                                                                    Streptavidin; ligand; binding affinity; mutant; isolation; purification; recover; immobilise; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HisaspThrPheThrLysValLysProSerAlaAlaSerIleAspAlaAl 167
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                                                                                                                                                                                                                                                                                                                                                                          (first entry)
Location/Qualifiers 50..601 /*tag= a
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Gaps: 0
Percent Identity: 100.000
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alignment_scores:
Quality:
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US-09-589-870-2 x V34714
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Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                   Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence encodes a wild-type streptavidin protein isolated from Streptomyces avidini. This sequence is used to produce mutants which are used in a method to assay the binding affinity of streptavidin mutants. These mutants have a mutation within the amino acid (aa) region 44-53 of the wild-type protein show a higher binding affinity than the wild-type for peptide ligands that include the sequence of formula Trp-X-His-pro-Gln-phe-Y-Z where X = any aa; Y and Z are both Gly, or Y = Glu and Z = Arg or Lys. Recombinant streptavidin mutants can be used to isolate, purify and determine proteins or to determine/recover substances that contain streptavidin-binding groups. Such compounds may also be used to immobilise fusions on microtitre plates, microbeads or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptavidin mutants with higher binding affinity for peptide ligands - have mutation in amino acid region 44-53, used to in purify or determine fusion proteins including these ligands
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sensor chips.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page -; 21pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Skerra A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-OCT-1996;
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                                                                               51
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                                                                                                                                                                                                                          alSerAlaAlaGluAlaGlyIleThrGlyThrTrpTyrAsnGlnLeuGly
                                                                                                                                                                   rIleThrAlaSerAlaSerAlaAspProSerLysAspSerLysAlaGlnV
rGluSerAlaValGlyAsnAlaGluSerArgTyrValLeuThrGlyArgT
                                                                             SerThrPheIleValThrAlaGlyAlaAspGlyAlaLeuThrGlyThrTy
                                                                                                           TCTCGGCCGCGAGGCCGGCATCACCGGCACCTGGTACAACCAGCTCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : This sequence does not appear in the specification but the mutant streptavidin sequence represented in V34715 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1998-218868/20
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/product=
                                                                                                                                                                                                                                                                                                                                                                                                                                              115 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              244 C; 193 G; 86 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                        Length:
Gaps:
Percent Identity:
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1 V34716.
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seq_documentation_block:
ID Z49867 standard; cDNA; 6:
XX
AC Z49867;
XY
DT 25-APR-2000 (first entr)
XX
Potato proteinase inhibit
XW potato proteinase inhibit
XX potato proteinase inhibit
XX proteinase in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name:
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  Disclosure; Fig 12; 111pp; English.
                                                        New chimeric polypeptide and composition comprising the useful for conferring pest resistance on plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         insect; plant-noxious protein; pest resistance; moth; insect; w
grub; beetle; fly; thrip; locust; cricket; borer; mite; looper;
insecticidal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potato proteinase inhibitor-II; PPI-II; streptavidin; worm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167
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                                                                                                                                                                                                                                                                                                                      HORTICULTURE & FOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene for recombinant pART27 vector
                                                                                                                                                                                                                                                                                                                                                                              98NZ-0331002
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122..598
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50..121
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                                                                                                                                                                                                                                                              Murray C,
                                                                                                                                                                                                                                                                    Markwick NP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       insect; weevil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167
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                                                                                     polypeptide
                                                                                                                                                                                                                                                              Philip BA;
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alignment_block:
US-09-589-870-2 x Z49867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes streptavidin, a plant-noxious protein. This is used in the preparation of a recombinant vector, pART27 designed to express a chimeric polypeptide comprising streptavidin mature peptide comprising streptavidin mature peptide. The fused to the potato proteinase inhibitor-II (PPI-II) signal peptide. The binary vector is targetted to the vacuole by PPI-II signal sequence. Transformation of plant genome with the vector can produce pest resistance in plants, plant derived products and stored harvest material. Pests that can be controlled include, cotton bollworm, coursel, plant genome corn-borer or rad miter tobacco horn worm, clopers, rice stem borer, porina, cutworms, diamondback moth, potato tuber moth, codling moth, Indian meal moth, gypsy moth, argentine stem weevil, clover root weevil, grass-grubs, corn rootworm, rice and wheat weevils, mealworms, flour beetles, black field cricket, locusts, sawflies, Western flower thrips, Hessian flies or two-spotted mite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: 249867
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                                                                                                                                         ValalaTrpLysAsnAsnTyrArgAsnAlaHisSerAlaThrThrTrpSe 117
                                                                                                                                                                                                                                                                                                                                                                                                                                              alSerAlaAlaGluAlaGlyIleThrGlyThrTrpTyrAsnGlnLeuGly
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GAAGAAGGCCGGCGTCAACAACGGCAACCCGCTCGACGCCGTTCAGCAG
                   aLysLysAlaGlyValAsnAsnGlyAsnProLeuAspAlaValGlnGln 183
                                                                                                                                                                                                                                                                                            CACGACACCTTCACCAAGGTGAAGCCGTCCGCCGCCTCCATCGACGCGGC
                                                                                         H1sAspThrPheThrLysValLysProSerAlaAlaSerIleAspAlaAl 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATTACGGCCAGCGCTTCGGCAGACCCCTCCAAGGACTCGAAGGCCCCAGG
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Ratio:
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alignment_block:
US-09-589-870-2 x N60626
                                                                                                alignment_scores:
Quality: 183.00
Ratio: 1.000
Percent Similarity: 100.000
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                                           Align seg 1/1
                                                                                                                                                                                                                                                                                 DNA sequences and hybrid DNA sequences - encoding streptavidin-like polypeptide, also joined to another protein, e.g. tissue plasminogen activator
The inventors claim the DNA sequence in SA307 which codes for a steptavidin-like polypeptide (see N60626), and the polypeptide encoded by it (P60625). They also claim hybrid SQs comprising a not a second sequence coding for another protein, polypeptide, and a second sequence coding for another protein, polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antiblotic; biotin binding affinity; fusion protein;
                     1 MetArgLysIleValValAlaAlaIleAlaValSerLeuThrThrValSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_2/gcgdata/geneseq/geneseqn/NA1986.DAT:N60626
                                                                                                                                                                                        econd sequence coding for another protein, polypeptide
or AA (pref. tissue plasminogen activator (TPA)).
                                                                                                                                                                                                                                                                                                                                P60623, P60624, P60625.
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6
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                                            N60626 from:
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/note= "P60623"
482..1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 481..1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= c
/product= streptavidin-like polypeptide
/note= "P60625"
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/note= "P60624"
                                                                                                                                                                                                                                                           54pp; English.
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                                                                                                Gaps:
: Identity:
                                            1131
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529
                     17
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17 rIleThrAlaSerAlaSerAlaAspProSerLysAspSerLysAlaGlnV 34

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seq_documentation_block:
ID z91074 standard; DNA;
XX
AC z91074;
XX
DT 06-JUN-2000 (first e
XX
DT 08-JUN-2000 (first e
XX
Plant somatic tissue
KW viability; mst gene;
XX
Plant somatic tissue
KW plant; ds.
XX
Plant somatic tissue
KW plant; ds.
XX
Plant plant; ds.
XX
Cos Streptomyces avidinii
XX
XX
Streptomyces avidinii
XX
XX
D0200007427-A2.
XX
D0200007427-A2.
XX
PD 17-FEB-2000.
XX
PD 17-FEB-2000.
XX
PD 17-FEB-2000.
XX
PD 30-JUL-1999; 99WO-1
XX
PD 30-JUL-1999; 99WO-1
XX
PD 03-AUG-1998; 98IL-(
XX
PD 03-AUG-1
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Degeneration of somatic plant tissue by expression of a heterologous protein, useful for controlling plant development and morphology, su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces avidinii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant somatic tissue viability; mst gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValAlaTrpLysAsnAsnTyrArgAsnAlaHisSerAlaThrThrTrpSe 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yrAspSerAlaProAlaThrAspGlySerGlyThrAlaLeuGlyTrpThr 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGACCTCCGGCACCACCGAGGCCAACGCCTGGAAGTCCACGCTGGTCGGC
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                                                                                                                                                                                                    Ginzberg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 degeneration; plant essential factor; deplet plant development; plant morphology; flower;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    depletion;
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alignment_scores:
   Quality:
                                                                                                          plant tissue by expressing a heterologous protein capable of binding a plant essential factor (PEF), in sommatic plant tissue cells, where heterologous protein expression causes depletion of the PEF so the plant viability is maintained, while simultaneous degeneration of the somatic plant tissue is effected. This sequence represents the Streptomyces avidinii mst gene as an example of a heterologous gene introduced into the plants. The methods can provide for the selective and optionally reversible cell degeneration in sommatic plant tissue. They can be used for artificially controlling plant development and morphology. They can be used e.g. to decrease the number of flowers in fruit producing plants so as to increase the number of fruits which reach maturity.
                                                                                                                                                                                                                                                                                                                                                                                                   The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as decreasing the number of flowers present to increase the number of fruit \boldsymbol{\cdot}
                                                                                                        Sequence 564 BP;
                                                                                                                                                                                                                                                                                                                                                                                                 relates to a method of effecting degeneration of a somatic
                                                                                                                                                                                                                                                                                                                                                                                                                                             85;
                                                                                                        109 A;
                  182.00
1.000
                                                                                                                                                                                                                                                                                                                                                                                                                                           91pp;
                                                                                                        213 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                             English
                                                                                                          169
                                                                                                        G
;:
                                                                                                        73 T; 0 other;
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Align seg 1/1 to: Z91074 from: ArgLysIleValValAlaAlaIleAlaValSerLeuThrThrValSerIl 18 ۳ to: 564 alignment\_block: US-09-589-870-2 x Z91074

Percent Similarity: 100.000

Percent Identity:

100.000

Gaps:

Ratio:

uSerAlaValGlyAsnAlaGluSerArgTyrValLeuThrGlyArgTyrA GTCGGCCGTCGGCAACGCCGAGAGCCGCTACGTCCTGACCGGTCGTTACG 85

ACCTTCATCGTGACCGCGGGGGGCGCCGACGGCCCTGACCGGAACCTACGA

213

214

89

85

spSerAlaProAlaThrAspGlySerGlyThrAlaLeuGlyTrpThrVal

. 101

164

264 AlaTrpLysAsnAsnTyrArgAsnAlaHisSerAlaThrThrTrpSerGl . 118 313

102 

364 413 135

463 151

GACACCTTCACCAAGGTGAAGCCGTCCGCCGCCTCCATCGACGCGGCGAA AspThrPheThrLysValLysProSerAlaAlaSerIleAspAlaAlaLy 168 513

168 sLysAlaGlyValAsnAsnGlyAsnProLeuAspAlaValGlnGln

GAAGGCCGGCGTCAACAACGGCAACCCGCTCGACGCCGTTCAGCAG 559

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seq_documentation_block:
ID 291076 standard; DNA;
XC 291076;
XX 291076;
XX 291076;
XX Plant somatic tissue
KW Plant plant; ds.
XX 203-0007427-A2.
XX 203-00007427-A2.
XX 203-0007427-A2.
XX 203-0007427-A2.
XX 203-00007427-A2.

                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-589-870-2 x Z91076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                  Align seg 1/1 to: Z91076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plant tissue is effected. This sequence represents the Streptomyces avidinii mprost gene as an example of a heterologous gene introduced into the plants. The methods can provide for the selective and optionally reversible cell degeneration in somatic plant tissue. They can be used for artificially controlling plant development and morphology. They can be used e.g. to decrease the number of flowers in fruit producing plants so as to increase the number of fruits which reach maturity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method of effecting degeneration of a somatic plant tissue by expressing a heterologous protein capable of binding a plant essential factor (PEF), in somatic plant tissue cells, where heterologous protein expression causes depletion of the PEF of the plant viability is maintained, while simultaneous degeneration of the somatic plant tissue is effected. This sequence represents the Streptomyces plant tissue is effected. This sequence represents the Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Degeneration of somatic plant tissue by expression of a heterologous protein, useful for controlling plant development and morphology, such as decreasing the number of flowers present to increase the number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Examples; Page 86-87; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces avidinii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plant somatic tissue degeneration; plant essential factor; depletion; viability; mprost gene; plant development; plant morphology; flower;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces avidinii mprost gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AGRI-) AGRIC RES ORG
                                        40
                                                                                                              11
                                                                                                                                                                                   24
yIleThrGlyThrTrpTyrAsnGlnLeuGlySerThrPheIleValThrA
                                                                                                                                                  AlaAspProSerLysAspSerLysAlaGlnValSerAlaAlaGluAlaGl 40
                                                                                                              GCTGACCCCTCCAAGGACTCGAAGGCCCAGGTCTCGGCCGCCGAGGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_2/gcgdata/geneseq/geneseqn/NA2000.DAT:Z91076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            495 BP; 98 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ginzberg
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                                                                                                                                                                                                                                                      from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 C;
                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 160
Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 T; 0 other;
                                        57
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seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1994.DAT:Q70659
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Q70659 standard; DNA; 1356 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                    New cpds. comprising a tagent of the compression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124
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                                               partic, tumour cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
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                                                                                                                                                                          WPI; 1994-248907/30
                                                                                                                                                                                                                           Deonarain M,
                                                                                                                                                                                                                                                                        (IMCR ) IMPERIAL CANCER RES
                                                                                                                                                                                                                                                                                                                         15-JAN-1993;
                                                                                                                                                                                                                                                                                                                                                                           17-JAN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CATCACCGGCACCTGGTACAACCAGCTCGGCTCGACCTTCATCGTGACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AsnGlyAsnProLeuAspAlaValGlnGln 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alLysProSerAlaAlaSerIleAspAlaAlaLysLysAlaGlyValAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACGGCAACCCGCTCGACGCCGTTCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGAAGCCGTCCGCCGCCTCCATCGACGCGGCGAAGAAGGCCGGCGTCAAC
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ng mammals f
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                                                                                                                                                                                                                                                                             TECHNOLOGY.
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                                                                      cytotoxic
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Claim 36; Fig 9; 114pp; English.

The sequence is that of the ECORI site obtd. by PCR. See also Q70652-69.

ScFv

pRAS108 and

pRAS112 between HindIII

and

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seq_documentation_block:
ID z91075 standard; DNA,
XX
AC z91075;
XX
O6-JUN-2000 (first of the text)
XX
DE Streptomyces avidini:
XX
Plant somatic tissue
KW viability; prost geno
KW viability; prost geno
KW fruit plant; ds.
XX
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US-09-589-870-2 x Q70659
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                              124
                               Plant somatic tissue degeneration; plant essential factor; depletion; viability; prost gene; plant development; plant morphology; flower;
                                                                                                                                                                                                                                                                    174
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                                                                           Streptomyces avidinii prost
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                                                                                                                                                                                                                                                                                                  TTAAGCCTTCTGCTAGCATTGATGCTGCCAAGAAAGCAGGCGTAAAC
                                                                                                                                                                                                                                                                                                                                                                         uAlaAsnAlaTrpLysSerThrLeuValGlyHisAspThrPheThrLysV 157
                                                                                                                                                                                                                                                                                                                                                                                                                   GCTGAGGCTCGTATCAACACTCAGTGGCTGTTAACATCCGGCACTACCGA 1214
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                                                                                                                                                                                                                                                                                                                                                           AGCGAATGCATGGAAATCGACACTAGTAGGTCATGACACCTTTACCAAAG
                                                                                                                                                                                                         /cgn2_2/gcgdata/geneseq/geneseqn/NA2000.DAT:Z91075
                                                                                                       (first entry)
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                                                                                                                                                                 DNA;
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Percent Identity:
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The invention relates to a method of effecting degeneration of a somatic plant tissue by expressing a heterologous protein capable of binding a plant essential factor (PEF), in somatic plant tissue cells, where heterologous protein expression causes depletion of the PEF so the plant viability is maintained, while simultaneous degeneration of the somatic plant tissue is effected. This sequence represents the Streptomyces avidinii prost gene as an example of a heterologous gene introduced into the plants. The methods can provide for the selective and optionally reversible cell degeneration in somatic plant tissue. They can be used for artificially controlling plant development and morphology. They can be used e.g. to decrease the number of flowers in fruit producing plants so as to increase the number of fruits which reach maturity.
                                                                                                                                                                                                                                                                                                                       Degeneration of somatic plant tissue by expression of a heterologous protein, useful for controlling plant development and morphology, such as decreasing the number of flowers present to increase the number of
                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; Y80514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-FEB-2000
Sequence 492
                                                                                                                                                                                                                                                                      Examples; Page 86; 91pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kapulnik Y, Ginzberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces avidinii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AGRI-) AGRIC RES ORG.
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 BP; 95
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 A;
 188
 Ç
 151 G; 58
 T; 0 other;
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alignment\_block: US-09-589-870-2 x Z91075 alignment\_scores: Quality: 159.00 Ratio: 1.000 Percent Similarity: 100.000 Align seg 1/1 to: 291075 from: Length: Gaps: Percent Identity: to: 100.000

110 60

91 260 108

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alignment_scores:
Quality:
                                   alignment_block:
US-09-589-870-2 x N80186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1988.DAT:N80186
                                                             Quality: 159.00
Ratio: 1.000
Percent Similarity: 100.000
                 Align seg 1/1 to: N80186
                                                                                                                                                                                                                                                                                                                                                                                                            Biosynthetic Antibody Binding site (BABS); variable domain; anti-CEA monoclonal antibody; streptavidin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              461
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                                                                                                                                          sequence.
See also N80171-N80192.
                                                                                                                                                                                                         Recombinant multifunctional protein having an antibody binding site and ion sequestering or binding to a so.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Encodes biosynthetic protein with streptavidin trailer
                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-OCT-1990 (first entry)
                                                                                                                                                           Encodes multi-functional biosynthetic protein comprising chain BABS and streptavidin protein trailer linked via a
                                                                                                                                                                                        Disclosure; ; 115pp; English.
                                                                                                                                                                                                                                                                                              (CREA-) CREATIVE BIOMOLECULES
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25 AspProSerLysAspSerLysAlaGlnValSerAlaAlaGluAlaGlyIl 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyAsnProLeuAspAlaValGlnGln 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oppermann
                                                                                                                                                                                                                                                                                                                87US-0052800.
                                                                                                                                                                                                                                                                                                                                  88WO-US01737.
                                                                                                                       117 A;
                  from: 1
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                                                             Length: 159
Gaps: 0
Percent Identity: 100.000
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                  ţo:
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                   498
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lid support.
                                                                                                                        111 T; 0
                                                                                                                         other
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                                                                                                                                                            single
spacer
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seq_documentation_block:
ID T75491 standard; DNA; 498 BP.
XX
AC T75491;
XX
DT 27-FEB-1998 (first entry)
XX
DNA for streptavidin.
XX
S-layer; sbs-A; vaccine; adjuve
KW molecular spinning nozzle; mole
XX
DE19603649-A1.
XX
PN DE19603649-A1.
XX
PN DE19603649-A1.
XX
O7-AUG-1997.
XX
O7-AUG-1997.
XX
VA
PR 01-FEB-1996; 96DE-1003649.
XX
PR 01-FEB-1996; 96DE-1003649.
XX
PR (LUBL/) LUBITZ W.
PA (SLEY/) SLEYTR U.
XX
PA (SLEY/) SLEYTR U.
XX
PR (LUBL/) LUBITZ W.
PA (SLEY/) SLEYTR U.
XX
PR (PARTAIN OF S-layer proteins
PT negative bacterium - or new sbs
PT recombinant proteins containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name:
Preparation of S-layer proteins by expressing sbs-A gene in Gram negative bacterium - or new sbs-B gene in any host, also new recombinant proteins containing heterologous inserts, e.g.
                                                                                                                                                                                                                                                                                                                                                                     S-layer; sbs-A; vaccine; adjuvant; carrier; hybridisation molecular spinning nozzle; molecular laser; streptavidin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    463
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epitope(s),

useful

as vaccines and adjuvants

FX 8 X 0 0 0 0 0 0 0 0 0 0 0 0 0 X 8 X 9

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seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1989.DAT:N90755
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                                    457
                                                                   175
                                                                                                    407
                                                                                                                                    158
                                                                                                                                                                   357
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                                                                                                                                                                                                                                                                                                                                                                                                     91
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                                                    GlyAsnProLeuAspAlaValGlnGln 183
                                                                                                                                                                   pGlySerGlyThrAlaLeuGlyTrpThrValAlaTrpLysAsnAsnTyrA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluSerArgTyrValLeuThrGlyArgTyrAspSerAlaProAlaThrAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lyAlaAspGlyAlaLeuThrGlyThrTyrGluSerAlaValGlyAsnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACTGGCACCTGGTATAACCAACTGGGGTCGACTTTCATTGTGACCGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eThrGlyThrTrpTyrAsnGlnLeuGlySerThrPheIleValThrAlaG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACCCGTCCAAGGACTCCAAAGCTCAGGTTTCTGCAGCCGAAGCTGGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AspProSerLysAspSerLysAlaGlnValSerAlaAlaGluAlaGlyI1
                                                                                                                                                                                                                                                                                                                                                                                                                                        GAATCCCGCTACGTACTGACTGGCCGTTATGACTCTGCCACCTGCCACCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGCGGACGGAGCTCTGACTGGCACCTACGAATCTGCGGTTGGTAACGCA
                                                                                                    AGCCTTCTGCTAGCATTGATGCTGCCAAGAAAGCAGGCGTAAACAAC
                                                                                                                      ysProSerAlaAlaSerIleAspAlaAlaLysLysAlaGlyValAsnAsn
                                                                                                                                                                                                                                                                                                                                                                        TGGCTCTGGTACCGCTCTGGGCTGGACTGTGGCTTGGAAAAACAACTATC
                                  GGTAACCCTCTAGACGCTGTTCAGCAA
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Ratio:
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Gaps:
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seq\_documentation\_block:

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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                     04-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                  N90755;
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                              N90755 standard;
                                                                                                                                                                                                                                                                                                                                                                                        chimeric
                                                                                                                                                                                                                                                                                                                                                                                                         streptavidin synthetic gene
                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                            synthetic gene; Streptomyces avidinii;
                                                                                                                                                                                                                                                                                  /label=BB217
87. 127
                                                                                                                                                                                                                                                                                                                                                         /*tag=
2..46
                                                                                                                                   /label=BB225
257..295
                       /label=BB231
381..423
                                                          399..380
                                                                                               296..338
                                                                                                                                                                      214...256
                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers 10..492
           /label=BB232
                /*tag=
                                               /label=BB230
                                                                                                                                                                                                                                                          /*tag=
                                                                /label=BB229
                                                                                   /label=BB228
                                                                                                                       /label=BB226
                                                                                                                                                                                                                                                                       /label=BB218
                                                                                                                                                                                                                                                                                                          /label=BB216
                                                                                                                                                                                                                                                                                                                                             /label=BB214
                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA;
     complement
                                   /*tag=
                                                                                                    'label=BB227
                                                                                                               complement
                                                                                                                                                          /label=BB224
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                                        complement
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     (390..431)
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                                                                                                                                                    (221..268)
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alignment_scores:
Quality: 159.00
Ratio: 1.000
Percent Similarity: 100.000
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US-09-589-870-2 x N90755
                                                                                                                                                                            Align seg 1/1 to: N90755
                                                                                                                                                                                                                                                                                                                              It is based upon the amino acid sequence of natural mature streptavidin (p93530). It is constructed from 24 oligomers (BB214-BB337) (see Features Table) which were synthesised by automated phosphoramidite chemistry. Complementary oligomers were annealed and the pairs ligated using T4 DNA ligase. The ligated product was sepd. and used to transform HM87. Plasmid DNA was isolated and positive clones selected. It has many restriction sites. Fragments of it are also claimed. The genetic construct is pref. a vector and comprises a chimeric gene composing all of a fragment of it fused to any other DNA sequence to result in a sequence encoding a hybrid protein with biotin-binding activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA sequence encoding streptavidin and comprising hybrid gene encoding fusion biotin-binding activity
                                    113
                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1989-130040/17.
P-PSDB; P93531.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-OCT-1988;
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                                 eThrG1yThrTrpTyrAsnG1nLeuG1ySerThrPheIleValThrAlag
                                                                                                                              GluSerArgTyrValLeuThrGlyArgTyrAspSerAlaProAlaThrAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; page 2/5; 22pp; English.
                                                                                                                                                                                                                                                                                                            507
                                                                                                                                                                                                                                                                                                            BP; 125
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466..502
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424..465
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                                                                                                                                                                                                                                                                                                           A; 137
                                                                                                                                                                              from: 1
                                                                                                                                                                                                                                      Percent Identity: 100.000
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             91
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seq_documentation_block:
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                      Streptavidin prodn. from Bacillus subtilis - using signal protein from bacterial exo-protein and expression element from Gram positive bacterial protein.
                                                                                                                                                                                                                                                                                   Key
CDS
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                                                                                                                                                                                                                                             sig_peptide
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                                                                                                                                                                                                                                                                                                                                Streptavidin;
                                                                                                                                                                                                                                                                                                                                                  Streptavidin gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108
      Disclosure; Fig 1b;
                                                              WPI; 1993-405822/50.
P-PSDB; R44491.
                                                                                                                                29-MAY-1992;
                                                                                                                                                 27-MAY-1993;
                                                                                                                                                                    09-DEC-1993
                                                                                                                                                                                                                                                                                                              Streptomyces avidinii.
                                                                                                                                                                                                                                                                                                                                                                                                          Q53412 standard; DNA;
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                                                                                                            (DUPO ) DU PONT
                                                                                                                                                                                       WO9324631-A
                                                                                                                                                                                                                                                                                                                                                                      27-JUN-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyAsnProLeuAspAlaValGlnGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rgAsnAlaHisSerAlaThrThrTrpSerGlyGlnTyrValGlyGlyAla 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTAACCCTCTAGACGCTGTTCAGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCCTTCTGCTAGCATTGATGCTGCCAAGAAAGCAGGCGTAAACAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pGlySerGlyThrAlaLeuGlyTrpThrValAlaTrpLysAsnAsnTyrA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAATCCCGCTACGTACTGACTGGCCGTTATGACTCTGCACCTGCCACCGA
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1..72
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73..519
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                                                                                                                                                                                                                 /*tag=
                                                                                                                                                                                                       note= "fused to npr signal peptide in pBE673"
      54pp; English
                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                secretion; Bacillus subtilis;
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portion

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seq_documentation_block:
ID Q70660 standard; DNA;
XX
AC Q70660;
XX
DT 26-MAR-1995 (first e
XX
DT 26-MAR-1995 and pRAS
XX
KW Amplification; single
XX
KW Amplification; Locat
XX
KW Locat
XX
KW Locat
XX
KW Locat
                                                                                                                                                                      seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1994.DAT:Q70660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179
                                                                       ScFV pRAS109 and pRAS113 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tetrameric biologically active streptavidin is produced by secretion from Bacillus subtilis transformed with a plasmid encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                    93
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Ratio: 1.000
Similarity: 100.000
                                                                                                                                                                                                       ProLeuAspAlaValGlnGln 183
                                                                                                                                                                                                                                                erAlaAlaSerIleAspAlaAlaLysLysAlaGlyValAsnAsnGlyAsn 176
                                                                                                                                                                                                                                                                                                                         rGlyThrAlaLeuGlyTrpThrValAlaTrpLysAsnAsnTyrArgAsnA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ArgTyrValLeuThrGlyArgTyrAspSerAlaProAlaThrAspGlySe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             spGlyAlaLeuThrGlyThrTyrGluSerAlaValGlyAsnAlaGluSer 76
                                                                                                                                                                                            CCGCTCGACGCCGTTCAGCAG
                                                                                                                                                                                                                                       CCGCCGCCTCCATCGACGCGGCGAAGAAGGCCGGCGTCAACAACGGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                              CGGCACCGCCTCGGTTGGACGGTGGCCTGGAAGAATAACTACCGCAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGCTACGTCCTGACCGGTCGTTACGACAGCGCCCCGGCCACCGACGGCAG
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                                                                                            (first entry)
                                                single chain variable region
      Location/Qualifiers
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                                                                                                                                       DNA;
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    used esp. for treat
partic. tumour cells

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used esp. for treating mammals for destroying target cells
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                                                                       AlaGluAlaArgIleAsnThrGlnTrpLeuLeuThrSerGlyThrThrGl 140
                                                                                                                  yrArgAsnAlaHisSerAlaThrThrTrpSerGlyGlnTyrValGlyGly 123
                                                                                                                                                 CGATGGCTCTGGTACCGCTCTGGGCTGGACTGTGGCTTGGAAAAACAACT 1114
                                                                                                                                                           rAspGlySerGlyThrAlaLeuGlyTrpThrValAlaTrpLysAsnAsnT 107
                                                                                                                                                                                            GCAGAATCCCGCTACGTACTGACTGGCCGTTATGACTCTGCACCTGCCAC
                   AGCGAATGCATGGAAATCGACACTAGTAGGTCATGACACCTTTACCAAAG
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194.884 Million cell updates/sec
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0; Mismatches 0; ADPSKDSKAQVSAAEAGITG	status predicted <sig> ttatus predicted <mand 183;="" 2;="" 7.4e-172;<="" db="" l="" no.="" pred.="" predicted="" score="" status="" td=""><td>iD:946740; PIDN:CAA27265.1; ek, м. inding sites of avidin and</td><td>nyces avidinii vision 03-Nov-1987 #text_change irken, S.; Axel, R.; Cantor, C. , 1986 cleotide sequence of the strep :86148514</td><td>STNAMNE</td><td>D83216 ELRT1 B49394 T00399 T00399 T08563 A75792 A756535 T08563 T08563 JC6535</td></mand></sig>	iD:946740; PIDN:CAA27265.1; ek, м. inding sites of avidin and	nyces avidinii vision 03-Nov-1987 #text_change irken, S.; Axel, R.; Cantor, C. , 1986 cleotide sequence of the strep :86148514	STNAMNE	D83216 ELRT1 B49394 T00399 T00399 T08563 A75792 A756535 T08563 T08563 JC6535
LGSTEIVTAGAD 60	183;	. PID:946741 streptavidin. Tyrosine res	nange 10-Dec-1999 c, C.R. streptavidin gene.	whie protein I - S translation elonga probable membrane probable translati pmbA protein - Esc probable initiator	probable aldolase pancreatic elastas translation elonga transcription fact beta-lactamase (EC probable acyl-coad dnay-related prote multiubiquitin-cha 26s proteinase (habitin synthase (E

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A; Title: Generation of new mutants of nmr, A; Reference number: Z23098; MUID:92035098
                                               R; Jarai, G.; Marzluf, G.A.
Curr. Genet. 20, 283-288, 1991
                                                                                        nitrogen metabolic regulation protein nmr [imported] - Neurospora crassa C;Species: Neurospora crassa C;Decies: Neurospora crassa C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 02-Sep-20C;Accession: T46600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Experimental source: strain Tue2605
C;Superfamily: streptavidin
F;1-24/Domain: signal sequence #status predicted
F;25-183/Product: streptavidin v2 #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Bayer, E.A.; Kulik, T.; Adar, R.; Wilchek, M. Biochin. Biophys. Acta 1263, 60-66, 1995
A;Title: Close similarity among streptavidin-like, A;Reference number: S57284; MUID:95359204
A;Accession: S57285
                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: S57285

Streptavidin v2 precursor - Streptomyces venezuelae C;Species: Streptomyces venezuelae C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 C;Accession: S57285
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C;Superfamily: streptavidin
F;1-24/Domain: sdignal sequence #status predicted <SIG>F;25-183/Product: streptavidin v1 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Bayer, E.A.; Kulik, T.; Adar, R.; Wilchek, M. Biochin. Biophys. Acta 1263, 60-66, 1995 A;Title: Close similarity among streptavidin-like, A;Reference number: S57284; MUID:95359204 A;Accession: S57284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-183 <BAY>
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A; Residues: 1-183 <BAY>
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C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 10-Dec-1999
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                                                                                                            02-Sep-2000
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Query Match
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R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and CA;Reference number: A81500; MUID:20150255
A; Gene: TC0347
C; Superfamily:
                                                                                                                                                        A; Reference number: A81500;
A; Accession: C81713
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                   C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Sep-2000
C;Accession: C81713
                                                                   A;Cross-references: GB:AE002302; GB:AE002160; NID:g7190382; PIDN:AAF39208.1; PID:g719
A;Experimental source: strain Nigg (MoPn)
                                                                                                                 A; Molecule type: DNA
A; Residues: 1-366 <TET>
                                                                                                                                                                                                                                                                                                                                                                                  DNA polymerase III, beta chain TC0347 [imported] - Chlamydia muridarum (strain Nigg)
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A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA polymerase III, beta chain CP0419 [imported] - Chlamydophila pneumoniae (strain A C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Sep-2000
C;Accession: F81578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE002203; GB:AE002161; A;Experimental source: strain AR39, HL cells
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A; Residues: 1-366 < REA>
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A;Status: preliminary; translated from
A;Molecule type: DNA
A;Residues: 1-212 <JAR>
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8; Conserv
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8; Conservative
  DNA-directed DNA polymerase
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100.0%; Pr.
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    beta chain
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                                                                                                                                                                                                                                                                       Heidelberg, J.F.; White, O.;
; Kolonay, J.; McClarty, G.; S
                                                                                                                                                                                                                              MoPn and Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 366;
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Salzbe
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4.48;

Score 8;

DB

2

Length 366;

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DNA polymerase III (beta chain) - Chlamydophila pneumoniae (strain CWL029) C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000 C:Accession: H72090
                                     RESULT
E71559
                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-367 <STO>
A;Cross-references: GB:AE004787; GB:AE004091; NID:g9949835; PIDN:AAG07065.1; GSPDB:GN001
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                             A;Title: Complete genome so
A;Reference number: A82950
A;Accession: B83186
A;Status: preliminary
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Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Date: 15-Sep-2000
C; Accession: 883186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable RND efflux membrane fusion protein precursor PA3677 [imported] - Pseudomonas ac
C; Species: Pseudomonas acruginosa
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C;Superfamily: DNA-directed DNA polymerase III beta
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A;Rosldues: 1-366 <ARN>
A;Rosldues: 1-366 <ARN>
A;Cross-references: GB:AE001618; GB:AE001363; NID:g4376610; PIDN:AAD18487.1; PID:g437661
A;Experimental source: strain CWL029
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A;Title: Comparative genomes of Clamydia pneumoniae and A;Reference number: A72000; MUID:99206606
A;Accession: H72090
A;Status: preliminary
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probable DNA pol III (beta chain)
C; Species: Chlamydia trachomatis
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Gene: PA3677
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Best Local Similarity 100
Matches 8; Conservative
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Matches 8; Conserv
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Best Local Similarity
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                                                                                                                                                                                4.48;
llarity 100.08;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence of Pseudomonas aeruginosa PA01, an
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                    Chlamydia
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6
                    trachomatis
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                    strain UW3/Cx)
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A;Status: not compared with conceptual translation A;Molecule type: DNA A;Residues: 1-488 <YOU>
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Best Local
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Best Local
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C;Accession: D75375

R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J., M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans Rl. A;Reference number: A75250; MUID:20036896

A;Accession: D75375

A;Accession: D75375

A;Accession: D75375

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-470 <a href="https://doi.org/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.1003/10.10
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R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R
Science 282, 754-759, 1998

A;Title: Genome sequence of an obligate intracellular pathogen
A;Reference number: A71570; MUID:99000809

A;Accession: E71559
nitrogen metabolic regulation protein nmr - Neurospora crassa N;Alternate names: nmr protein C;Species: Neurospora crassa C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: S11910; S11924 R;Young, J.L.; Jarai, G.; Fu, Y.H.; Marzluf, G.A. Mol. Genet. 221, 120-128, 1990 Mol. Genet. 221, 120-128, 1990 A;Reference number: S11910; MUID:91042412 A;Accession: S11910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
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C;Superfamily: DNA-directed DNA polymerase III beta
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A;Experimental source: serotype I
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A; Residues: 1-416 <ARN>
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nilarity 100.08;
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D, strain UW-3/Cx
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A; Gene: nmr
C; Superfamily: nitrogen metabolic regulation protein
C; Keywords: nucleus; transcription regulation
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                                                                                                                                                                                                                                                                                                                                                                          C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000
C;Accession: E81051
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A;Accession: G81825
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                                                                                       A;Gene: NMB1715
C;Superfamily: acriflavin
                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-1067 <TET>
A;Cross-references: GB:AE002521;
A;Experimental source: serogroup
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C;Superfamily: acriflavin
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A; Residues: 1-1067 <PAR>
A; Cross-references: GB:AL162757;
A; Experimental source: serogroup
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Query Match
Best Local Similarity
Matches 87 Conserv
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Best Local (
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nes 8; Conser
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nilarity 100.0%;
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b; Pred. No. 7.7
0; Mismatches
       0,
                                                                                                                                             GB:AE002098; NID:g7226962; PIDN:AAF42062.1; PID:g72269
B, strain MMD58
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       Score 8; DB 2; Pred. No. 15; 0; Mismatches
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Pred. No.
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5. 7.7;
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erty, B.A.
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A:Gene: S
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S59969
                                                                                                                                                              A; Map position: 93.16-93.82
C; Superfamily: phage lambda
C; Keywords: host cell lysis
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A; Residues: 1-107 <SAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-107 < DAN>
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A; Accession: H94164
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C; Species: pha
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A; Residues: 1-1612 <DER>
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C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 15-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999
C;Accession: S59969; S54154
R;Dereuddre, S.; Frey, S.; Delaporte, C.; Jacquemin-Sablon, A.
Biochim. Biophys. Acta 1264, 178-182, 1995
A;Title: Cloning and characterization of full-length cDNAs coding for the DIA; Reference number: S59969; MUID:96085121
A;Accession: S59969
                                                                                                                                                                                                A:Experimental source: lung (ATP-C)Superiamily: eukaryotic type II DNA topoisomerase; phage T4 DNA topoisomerase (ATP-C)Superiamily: eukaryotic type II DNA topoisomerase; nucleus C:Keywords: ATP: DNA binding; DNA replication; isomerase; nucleus F:697-927/Domain: phage T4 DNA topoisomerase (ATP-hydrolyzing) medium chain homology
                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X86455; NID:g790987; PIDN:CAA60173.1; PID:g790988
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September 1982

C;Species: phage lambda
C;Date: 13-Jun-1983 #sequence\_revision 13-Jun-1983 #text\_change 23-Jul-1999
C;Accession: H94164; G43012; A04327 D.F.;

A;Cross-references: GB:J02459; GB:M17233; GB:M24325; GB:V00636; GB:X00906; NID:g21510 A;Note: the lambda DNA sequence is from the standard strain lambda-cIindlts857Sam7; t

0; Length 107 Indels 0; Gaps 0,

Search completed: April 6, 2001, 01:26:46 Job time: 1180 sec

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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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INVOLVED IN BIOTIN BINDING.
CELL ATTACHMENT SITE.
4652D8AE018468F5
 CRC64;
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Query Match
Best Local Similarity
Matches 183; Conserv

100.0%; ilarity 100.0%; Conservative C

0;

Score 183; DB 1; Pred. No. 1.5e-177; ); Mismatches 0;

Length 183; ; Indels

0;

Gaps

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60

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RESULT
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                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                        BIOCHIM. BLOPHYS. ACTA 1263-60-66(1995).

-I- FUNCTION: THE BIOLOGICAL FUNCTION OF STREPTAVIDIN FORMS A STRONG NON-COVALENT SPECIFIC COMPLEX WITH MOLECULE OF BIOTIN PER SUBUNIT OF STREPTAVIDIN).
                                 SEQUENCE
                                                     BINDING
                                                                           BINDING
                                                                                                 BINDING
                                                                                                                    BINDING
                                                                                                                                          BINDING
                                                                                                                                                                Signal; Biotin
                                                                                                                                                                                                                   EMBL; S78777; AAB35015.1;
HSSP; P22629; 1PTS.
                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95359204; PubMed-7632734;
Bayer E.A., Kulik T., Adar R., Wilchek M.;
"Close similarity among streptavidin-like,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces violaceus (Streptomyces venezuelae). Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                  PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                           INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
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                                                                                                                                                                                                                                                                                                                                        SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
SUBCELLULAR LOCATION: SECRETED.
SIMILARITY: BELONGS TO THE AVIDIN/STREPTAVIDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                    se similarity among Streptomyces.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VQQ 183
                                                                                                                                                                                                PF01382;
                                                                                                                                                                                      01382; Avidin;
PS00577; AVIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183
                                                                                                                                                                                                 IPR000088; -.
                                 183
                                                     144
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25
67
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                                 A,
                                                                                                                                                                                    AVIDIN;
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183
67
                                 18864
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                                                                                  BY SIMILARITY.
STREPTAVIDIN VI.
INVOLVED IN BIOTIN B
SIMILARITY).
 Score
                                           SIMILARITY
                                                                SIMILARITY)
                                                     INVOLVED IN BIOTIN
                                                                          INVOLVED IN BIOTIN
                                 4652D8BB14847DE0
 123;
 В
                                                                                                                                                                                                                                                                                                                                                                                                                              biotin-binding
Length 183;
                                                                                                                                          BINDING
                                 CRC64;
                                                                           BINDING
                                                                                               BINDING
                                                                                                                    BINDING
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RESULT 3
SAV2_STRVL
ID SAV2_STRVL
AC Q53533;
DT 01.NOV-1997
DT 01.NOV-1997
DT 15-JUL-1999
DE STREPTAVIDIT
OS ACTINOMYCETE
RN [1]
OR ACTINOMYCETE
RN [1]
RT CLOSE SIMILAM-953;
RA BAYET E.A.,
RT "CLOSE SIMILAM-953;
RA BAYET E.A.,
RT 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochim. Biophys. Acta 1263:60-66(1995).

-!- FUNCTION: THE BIOLOGICAL FUNCTION OF STREPTAVIDIN IS NO FORMS A STRONG NON-COVALENT SPECIFIC COMPLEX WITH BIOTI MOLECULE OF BIOTIN PER SUBUNIT OF STREPTAVIDIN).

-!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: SECRETED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
STREPTAVIDIN V2 PRECURSOR (SA V2)
                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; S78782; AAB35016.1; -. HSSP; P22629; 1PTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Close similarity among streptavidin-like, biotin-binding proteins from Streptomyces.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-95359204; PubMed-7632734;
Bayer E.A., Kulik T., Adar R., Wilchek M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces violaceus (Streptomyces venezuelae).
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                                                                                                                                                                                                                                                                                                                                                       PF01382;
                                                                                                                                                                                                                                                                                                         Biotin.
                                                                                                                                                                                                                                                                                                                             PS00577; AVIDIN; 1.
                                                                                                                                                                                                                                                                                                                                                                           529; 1PTS.
IPR000088; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Firmicutes; Actinobacteria; Actinobacteridae;
  183
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67
  A,
                                                                                                                                                                                                                                                                                                                                                       Avidin;
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183
67
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SIMILARITY).
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                                                INVOLVED IN BIOTIN
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; Mismatches
  FEAFFFFFFEA4 ECCA
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  CRC64;
                                                BINDING
                                                                                            BINDING
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Query Match 32.2%; Strest Local Similarity 100.0%; Matches 59; Conservative 0;

Score 59; DB 1; Pred. No. 3.1e-9 0; Mismatches

.1e-52;

Indels

0

Gaps

0

Length 183

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63

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                                                                                                                         RESULT 4
NMR_NEUCR
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                                                   Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                          "Analysis of conventional and in vitro generated mutants of nmr, the negatively acting nitrogen regulatory gene of Neurospora crassa.";

MOI. Gen. Genet. 222:233-240(1990).

-i- FUNCTION: MAJOR NEGATIVE REGULATORY PROTEIN IN THE NITROGEN CONTROL CIRCUIT OF NEUROSPORA CRASSA WHICH ALLOWS UTILIZATION
                                                                                                                                                                                                                                                    PIR;
                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restructed the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NMR_NEUCR STANDARD; PRT; 488 AA P23762; 01-NOV-1991 (Rel. 20, Created) 01-NOV-1991 (Rel. 20, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation updat
                                                                                                                         SEQUENCE
                                                                                                                                                    SIMILAR
                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Generation of new mutants of nmr, the negative-acting nitrogen regulatory gene of Neurospora crassa, by repeat induced mutation."; Curr. Genet. 20:283-288(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol.
                                                                                                                                       DOMAIN
                                                                                                                                                                                MUTAGEN
                                                                                                                                                                                                           MUTAGEN
                                                                                                                                                                                                                         Nuclear
                                                                                                                                                                                                                                    Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jarai G., Marzluf G.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91109706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=74-OR23-1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 99-310 FROM N.A. MEDLINE=92035098; PubMed=1834354; Jarai G., Marzluf G.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Young J.L., Jarai G., Fu Y.H., Marzluf G.A.; "Nucleotide sequence and analysis of NMR, a negative-acting regulatory gene in the nitrogen circuit of Neurospora crassa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=74-OR23-1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NITROGEN METABOLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91042412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neurospora crassa
                        165 DAAKKAGV 172
161 DAAKKAGV 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                                   OF VARIOUS NITROGEN-CONTAINING COMPOUNDS. SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
                                                                                                                                                                                                                                                   S11910; S11910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gen. Genet. 222:120-128(1990).
                                                                                                                                                                                                                                                                S64286; CAB32318.1;
                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                 non-profit institutions as long
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                                                                                                                         488
                                                                                                                                                                              386
386
                                                    Conservative
                                                                                                                                                    96
                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=2146484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=2148799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGULATION PROTEIN (NMR PROTEIN).
                                                                                                                                       488
                                                                                                                                                    193
                                                                                                                                                                              386
386
                                                                                                                         54857
                                                                 4.4%;
                                                                                                                         ₩:
                                                                                                                                                                                                                                    Repressor; Nitrate assimilation;
                                                      0:
                                                                 Score 8; I
; Pred. No.
                                                                                                                        TO YEAST ARGRII (AA 588-681).
DISPENSABLE FOR NMR FUNCTION.
; DODAF91671C7846C CRC64;
                                                                                                                                                              G->D,R: LOSS OF FUNCTION.
G->C,S: FEW, VERY SLOWLY GROWING
TRANSFORMANTS.
                                                                                                                                                                                                           P->K: LOSS OF FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sordariales; Sordariaceae; Neurospora.
                                                    Mismatches
                                                                 DB 1;
. 2.6;
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                                                                                                                                                                                                                                                                                                                                                              a collaboration
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                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the
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RESULT VLYS\_LAMBD

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RESULT 5
TP2B_CRILO
ID TP2B_CRILO
ID TP2B_CRILO
AC Q64399
DT 15-UUL
DT 15-UUL
DT 15-UUL
DT 30-MAX
DE EUKARI
OC GN TOP2B.
OS Cricet
RN FISSUE
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15-JUL-1998
30-MAY-2000
                                                                                                                                                                                                                                                                                NP_BIND
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00204; DNA_topoisoII; PFAM; PF00521; DNA_topoisoIV; PRINTS; PR00418; TPI2FAMILY. PRINTS; PR00615; CCAATSUBUNTA. PRINTS; PR01158; TOPISMRASEII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochim. Biophys. Acta 1264:178-182(1995)
11- FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY
EREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS.
MAKES DOUBLE-STRAND BREAKS.
11- CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAG
OF DOUBLE-STRANDED DNA.
11- SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X86455;
HSSP; P06786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96085121; PubMed=7495861;
Dereuddre S., Frey S., Delaporte C., Jacquemin-Sablon A.;
"Cloning and characterization of full-length cDNAs coding for the
                                                                                                                                                                                                                                                Isomerase; Topoisomerase; DNA-binding; ATP-binding; Nuclear protein.
NP_BIND 170 175 ATP (POTENTIAL).
ACT_SITE 814 B14 DNA CLEAVAGE (BY SIMILARITY).
SEQUENCE 1612 AA; 182074 MW; COID6FC40620FC68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERPRO; IPRO01154; -.
INTERPRO; IPRO01241; -.
INTERPRO; IPRO02205; -.
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                                                    57 AGADGALT 64
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MISCELLANBOUS: EUKARYOTIC TOPOJSOMERASE I AND II CAN
NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS PROKARYOTI
RELAX ONLY NEGATIVE SUPERCOILS.
SIMILARITY: BELONGS TO TYPE II TOPOISOMERASE FAMILY.
AGADGALT
                                                                                                           Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                              PS00177; TOPOISOMERASE_II; 1.
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(Rel. 36, Last sequence update)
(Rel. 39, Last annotation update)
MERASE II, BETA ISOZYME (EC 5.99.1.3).
                                                                                                           llarity 100.0%;
Conservative
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                                                                                                                                     Score 8;
Pred. No
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DNA CLEAVAGE (BY SIMILARITY)
MW; C01D6FC40620FC68 CRC64;
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JYL BPP22
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JY 01-MAR-1989 (Rel. 10, Created)
JY 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-MAR-1989 (Rel. 40, Last annotation update)
DT 01-CT-2000 (Rel. 40, Last annotation update)
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Sanger F., Coulson A.R., Hong G.F., Hill D.F.,
"Nucleotide sequence of bacteriophage lambda Di
J. Mol. Biol. 162:729-773(1982).
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21-JUL-1986 (Rel.
01-OCT-2000 (Rel.
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HOLIN (GPS PROTEIN) [INCLUDES: LYSIS PROTEIN S;
  Viruses; dsDNA viruses,
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7; Conser
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RNA stage; Tailed phages; Podoviridae
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POTENTIAL.
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Matches 7
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                                                                                                           MEDLINE-90133967; PubMed-2533272;
Ohama T., Muto A., Osawa S.;
"Spectinomycin operon of Micrococcus luteus: evolutionary implications of organization and novel codon usage.";
J. Mol. Evol. 29:381-395(1989).
-i- FUNCTION: BINDS DIRECTLY TO THE CENTRAL DOMAIN OF 165
             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                              01-OCT-1993 (Rel. 27, Created)
01-NOV-1995 (Rel. 32, Last seq
01-NOV-1995 (Rel. 32, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M10997; AAA32265.1; -.
EMBL; X67137; CAA47616.1; -.
EMBL; AF217253; AAF75039.1; -.
PIR; S22903; YVBPS2.
Phage lysis protein; Late protein.
Phage lysis protein; Late protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-slb.ch).
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"The completed sequence of genome of Salmonella phage P22.";
Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: ESSENTIAL FOR LYSIS OF THE BACTERIAL CELL WALL BY
DISRUPTING THE CELL MEMBRANE, THEREBY GIVING HYDROLYTIC ENZYMES
ACCESS TO THE CELL WALL.
-!- SIMILARITY: BELONGS TO THE LAMBDA PHAGE S PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Schicklmaier P., Huber J., Schmieger H.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                             Micrococcus luteus (Micrococcus lysodeikticus).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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"Phage P22 lysis genes: nucleotide sequences
relationships with T4 and lambda genes.";
Virology 143:280-289(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
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                                                                                                                                                                                                                                              Actinomycetales; Micrococcineae;
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                                                                                SIMILARITY: BELONGS
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А.
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are no res
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Best Local 9
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Ol-NOV-1991 (Rel. 20, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
SUPEROXIDE DISMUTASE (CU-ZN] 4A (EC 1.15.1.1).
SODEC.3 OR SOD4A.
Zea mave (Martin)
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                 PRINTS; PRO0068; CUZNDISMTASE.
PROSITE; PS00087; SOD_CU_ZN_1; 1.
PROSITE; PS00332; SOD_CU_ZN_2; 1.
Oxidoreductase; Copper; Zinc; Mul'
                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cannon R.E., Scandalios J.G.;
"Two cDNAs encode two nearly identical Cu/Zn superoxide dismutase proteins in maize.";
Mol. Gen. Genet. 219:1-8(1989).
-!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
-!- CALLYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).
                                                                                       PFAM; PF00080; sodcu; 1.
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
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01-NOV-1991
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                                                                                                                                 MENDEL; 299;
                                                                                                                                                                      HSSP; P07505; 1SRD.
                                                                                                                                                                                       PIR; S07007; S07007.
                                                                                                                                                                                                      EMBL; X17564; -; NOT_ANNOTATED_CDS
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nes 7; Conser
                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collab ween the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                     MISCELLANEOUS: EUKARYOTIC CELLS CONTAIN A MITOCHONDRIAL MN-CONTAINING ENZYME & A CYTOPLASMIC CU-ZN-CONTAINING ENZYME PLANT ALSO HAVE A CHLOROPLAST CU-ZN ENZYME.
                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE CU-ZN SUPEROXIDE DISMUTASE FAMILY
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$7; $29885; $29885.

$RPRO; IPRO00630; -
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                                                                                                                               ZEAma; SodCc; 3.
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100.0%;
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                                                                                        PRINTS; PRO0068; CUZNDISMTASE.
PROSITE; PS00087; SOD_CU_ZN_1;
PROSITE; PS00332; SOD_CU_ZN_2;
Oxidoreductase; Copper; Zinc; N
                                                                                                                                                                                                          MAIZEDB; 47586; -. MENDEL; 298; ZEAma
                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Two cDNAs encode two nearly identical Cu/Zn superoxide proteins in maize.";
MO1. Gen. Genet. 219:1-8(1989).
-i- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
-i- CATALTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = 0(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=90136495; PubMed=2482436;
Cannon R.E., Scandalios J.G.;
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
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01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
SUPEROXIDE DISMUTASE [CU-ZN] 4AP (EC 1.15.1.1).
SODCC.2 OR SOD4AP.
                                                                                                                                                                    PFAM; PF00080; sodcu; 1.
                                                                                                                                                                                                                                                                  EMBL; x17565; -; NOT PIR; S07008; S07008.
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MISCELLANEOUS: EUKARYOTIC CELLS CONTAIN A MITOCHONDRIAL
MN-CONTAINING ENZYME & A CYTOPLASMIC CU-ZN-CONTAINING E
PLANT ALSO HAVE A CHLOROPLAST CU-ZN ENZYME.
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COPPER (BY SIMILARITY).
COPPER AND ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
COPPER (BY SIMILARITY).
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COPPER AND ZINC (BY SIMILARITY).
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Pred. No.
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Matches 7
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INTERPRO; IPR00124; -.
PFAM; PF00080; sodcu; 1.
PRINTS; PR00068; CUZNDISMTASE.
PROSITE; PS00087; SOD_CU_ZN_1; 1.
PROSITE; PS00332; SOD_CU_ZN_2; 1.
PROSITE; PS00332; Copper; Zinc; Acety
                    Oxidoreductase;
INIT_MET 0
MOD_RES 1
METAL 45
METAL 47
METAL 47
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Wolf B., Reinecke K., Aumann K.-D., Brigelius-Flohe R., Flohe L.;
"Taxonomical classification of the guinea pig based on its Cu/Zn
superoxide dismutase sequence.";
Biol. Chem. Hoppe-Seyler 374:641-649(1993).
Biol. Chem. Hoppe-Seyler 374:641-649(1993).
-I- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
-I- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).
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P33431;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a copyred the swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict the propens and the swiss Institutions as long as its content is used by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O1-FEB-1994 (Rel. 28, Created)
O1-FEB-1996 (Rel. 33, Last sequence update)
O1-FEB-1996 (Rel. 33, Last annotation update)
SUPEROXIDE DISMUTASE (CU-ZN) (EC 1.15.1.1).
                                                                                                                                                                                                                                                                                           PIR; S36108; S36108.
                                                                                                                                                                                                                                                                                                                  EMBL; U39844; AAC52720.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: HOMODIMER.
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7: Conserv
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ZINC (BY SIMILARITY).
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Hystricognathi; Caviidae; Cavia.
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P00733;

21-JUL-1986 (Rel. 0

01-FEB-1995 (Rel. 3

30-MAY-2000 (Rel. 3
                                                                                                                   WERY J.-P., Charlier P., Dideberg O.;
Submitted (MAR-1996) to the PDB data bank.

-i- FUNCTION: THIS ENZYME CATALYZES CARBOXYPEDTIDATION AND
TRANSPEPTIDATION REACTIONS INVOLVED IN MACTERIAL CELL WALL
METABOLISM. IT EFFECTIVELY CATALYZES THE TRANSFER OF THE N-ALPHA,
N-EPSILON-DIACETYL-L-LYSYL-D-ALANYL ELECTROPHILIC GROUP OF THE
STANDARD TRIPEPTIDE SUBSTRATE N-ALPHA, N-EPSILON-DIACETYL-L-LYSYL-
D-ALANYL-D-ALANINE TO MATER. IT ALSO PERFORMS A WEAK BETA-
LACTAMASE ACTIVITY, HYDROLYSING PENICILLIN INTO PENICILLOATE AT A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METAL
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
MURAMOYL-PENTAPEPTIDE CARBOXYPEPTIDASE PRECURSOR (EC 3.4.17.6
(METALLO DD-PEPTIDASE) (ZN DD-PEPTIDASE) (D-ALANYL-D-ALANINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete amino acid sequence of alanine-cleaving carboxypeptidase of cur. J. Biochem. 130:53-69(1983).
                                                                                                                                                                                                                                                                                                                                                                                                       "Structure of a Zn2+-containing D-alanyl-D-alanine-cleaving carboxypeptidase at 2.5-A resolution.";
Nature 299:469-470(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS)
MEDLINE-83012968; PubMed-7121588;
Dideberg_O., Charlier P., Dive G., Jor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces albus G. Bacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METAL
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MEDLINE=83131648; PubMed=6825689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encoding
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- CATALYTIC ACTIVITY: HYDR
BOND IN PEPTIDOGLYCAN.
- COFACTOR: ZINC.
- SUBCELLULAR LOCATION: SE
- PTM: THE N-TERMINUS IS P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            van Beeumen J.,
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Pred. No. 9.5
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Hydrolase; Carboxypeptidescription
                                                                          SEQUENCE FROM N.A.

MEDLINE=85054882; PubMed=6094548;

Swift G.H., Craik C.S., Stary S.J.,

Rutter W.J., Macdonald R.J.;
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P00773;
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            pancreas.",
J. Biol. Cl
                                                                                                                                                                                                   "Primary structure of two distinct determined by sequence analysis of ribonucleic acid sequences.";
Biochemistry 21:1453-1463(1982).
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21-JUL-1986 (Rel.
15-JUL-1999 (Rel.
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                                                                                                                                                                                                                                                                                                   Nikovits W., Rutter W.J.;
                                                                                                                                                                                                                                                                                                                       MEDLINE=82182967; PubMed=6918221; McDonald R.J., Swift G.H., Quinto
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
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                                                        *Structure of the two related elastase
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Biol. Chem. 259:14271-14278(1984).
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URSOR (EC 3.4.21.36).
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EMBL; LO0113; AAA98811.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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SIGNAL
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PRINTS; PR00722; CHYMOTRYPSIN.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE OF 17-45.
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CATALYTIC ACTIVITY: HYDROLYSIS OF PROTEINS,
PREFERENTIAL CLEAVAGE: ALA-| XAA.

SUBCELLULAR LOCATION: SECRETED.

TISSUE SPECIFICITY: PANCREAS.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1;
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VGGAEAR
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-1- CATALYTIC ACTIVITY: L-ASPARTATE 4-SEMIALDEHYDE + PYRUVATE - DIHYDRODIPICOLINATE + 2 H(2)0.
-1- ENZYME REGULATION: SENSITIVE TO LYSINE INHIBITION
SEQUENCE FROM N.A.

MEDLINE-98172730; PubMed=9511739;

MEDLINE-98172730; PubMed=9511739;

Pusch W., Jaehner D., Ivell R.;

"Molecular cloning and testicular expression of the gene transcripts

encoding the murine multiubiquitin-chain-binding protein (Mcbl).";
                                                                                                                                                                                                                                                                       PSMD4 OR MCB1.
Mus musculus (Mouse).
Eukaryota; Metazoa; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM, PF00701; DHDPS; 1.

PRINTS; PR00146; DHPICSNTHASE.

PROSITE; PS00665; DHDPS_1; 1.

PROSITE; PS00666; DHDPS_2; 1.

Lyase; Diaminopimelate biosynthesis; Lysine biosynthesis;
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INTERPRO; IPRO02220; -.
PFAM: BECOTTO
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-I- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF DIAMINOPIMELATE AND LYSINE FROM ASPARTATE SEMIALDEHYDE.
-I- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
-I- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-I- SIMILARITY: BELONGS TO THE DHDPS FAMILY.
                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
26s PROTEASOME REGULATORY SUBUNIT S5A (MULTIUBIQUITIN CHAIN BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z68126; CAA92211.1; -. HSSP; P05640; 1DHP.
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31769 MW;
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35 SAAEAGI 41
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242 SAAEAGI 248
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                                                                                                                                                                     EMBL; AF013099; AAC53547.1; -. MGD; MGI:1201670; PSMD4.
                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
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-!- SIMILARITY: BELONGS TO THE PROTEASOME SUBUNIT S5A FAMILY.
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7; Conserv
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 Mismatches

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sp_bacteria:*
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O9m888 arabidopsis
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O9pkw4 chlamydia p
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O9k274 chlamydia p
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O9y9006 trichoderma
O9r278 deinococcus
O9jy67 neisseria m
O9y151 neisseria m
O9wf8 xanthomonas
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## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CV. COLUMBIA;
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Barnstead M.E.,
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC F13E7 genomic sequence.";
"Arabidopsis thaliana chromosome III BAC F13E7 genomic sequence.";
"Arabidopsis thaliana chromosome III BAC F13E7 genomic sequence.";
"BMBL; AC018363; AAF786973.1;
"EMBL; AC018363; AAF786973.1;
"SEQUENCE 271 AA; 29121 MW; 278584BF541B8F5F CRC64;
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

Brassicales; Brassicaceae; Arabidopsis.
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Matches 8
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AE002301; AAF39208.1; -.

TIGR; TC0347; -.
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Q9PKW4;
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STRAIN-MOPN / NIGG;
MEDLINE-20150255; PubMed-10684935;
MEDLINE-20150255; PubMed-10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.
Gwinn M., Nelson W., DeBby R., Kolonay J., McClarty G., Salzberg
Elsen J., Fraser C.M.;
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Bacteria; Chlamydiales;
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                                                                                                                                                                                                                            PFAM; PF00712;
SEQUENCE 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids
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Bacteria; Chlamyd
NCBI_TaxID=83558;
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                                                                                                                                                                                                                                                                                       INTERPRO;
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                                                                                            Local
   75 ESRYVLTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESRYVLTG
                                                                 Similarity
8; Conserv
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8; Conservative
                                                                                                                                                                                                                                                                                           IPR001001; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pneumoniae (Chlamydophila pneumoniae).
Chlamydiales; Chlamydiaceae; Chlamydophila.
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 15, Last annotation update)
ASE III, BETA SUBUNIT.
                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                            DNA_pol3_beta;
AA; 40493 MW;
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AA; 40334 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28:1397-1406(2000).
                                                    4.4%; 500
100.0%; Pr
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100.0%; Pr
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                                                                                            Score 8;
Pred. No
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8A6D188DB26BC5E1 CRC64;
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E3887C463C442D72 CRC64;
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Mismatches
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10;
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                                                                                                                         Length 366;
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                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              White 0.,
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Best Local S
Matches 8
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Best Local Similarity
Matches 8; Conser
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01-OCT-2000
01-OCT-2000
01-OCT-2000
                                                                                                                                                                                                                   Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumo from Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314 (2000).

EMBL; APO02546; BAA98548.1; -.

SEQUENCE 366 AA; 40364 MW; EBFA92ACF76BD1B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9JSG3;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
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Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Umayam L.A., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay C., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation updat
DNA POLYMERASE III, BETA SUBUNIT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=83558;
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydo
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Nucleic Acids Res. 28:1397-1406(2000).
  149
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ESRYVLTG
                                                ESRYVLTG 82
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8; Conser
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100.0%;
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                                                                                                                      Score 8; I Pred. No.
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Pred. No.
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.A., Utterback T.,
ouri H., Craven B.,
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                                                                                                                                             Length 366
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                                                                                               Indels
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Matches 8
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Matches 8; Conserv
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Q99006;
01-NOV-1996
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084078;
01-NOV-1998
                                                                                                                                                         INTERPRO; IPRO01223; -.
INTERPRO; IPRO01579; -.
PFAM; PF007704; Glyco_hydro_18; 1.
PROSITE; PS01095; CHITINASE_18; 1
Hydrolase; Glycosidase.
SEQUENCE 428 AA; 46881 MW; 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fekete C., Weszely T., Hornok L.; "Assignment of a PCR-amplified chitinase sequence cloned Trichoderna hamatum to resolved chromosomes of potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis."; Science 282:754-759(1998).
EMBL; AE001282; AAC67666.1; -.
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MEDLINE-99000809; PubMed-9784136;
Stephens R.S., Kalman S., Lammel C.J., Fallichell W.P., Olinger L., Tatusov R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNAN.
Chlamydia trachomatis.
Bacteria: Chlamydiales; Chlamydiaceae; Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                          species of Trichoderma." FEMS Microbiol. Lett. 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fung1; Ascomycota; anamorphic Ascomycota; Trichoderma. NCBI_TaxID-49224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-TAM-61
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PF00712; DNA_pol3_beta;
NCE 416 AA; 46529 MW;
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(TrEMBLrel. 13,
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01-MAY-2000
01-JUN-2000
                   Tettelin H., Saunders N.J., Heldelberg J., Jeffries A.C., Nelson K.E. Elsen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Clecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappublik, Venter J.C.;
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-MC58 / SEROGROUP B;
MEDLINE-20175755; Pubmed-10710307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
MULTIPLE TRANSFERABLE RESISTANCE SYSTEM PROTEIN MTRD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D. Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
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01-MAY-2000 (TEEMBLrel. 13, Last sequence update)
01-JUN-2000 (TEEMBLrel. 14, Last annotation update)
CONSERVED HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis (serogroup Bacteria; Proteobacteria; beta sub
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SEQUENCE 470 AA;
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Bacteria; Thermus/Deinococcus
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Best Local :
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Q9WWF8;
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Q9JT51;
01-OCT-2000
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Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd
Jagels K., Leather S., Moule S., Munlel K., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.;
"Complete DNA sequence of a serogroup A strain of Neisseria
menigitidis Z2491.";
Nature 404.502-506(2000).
EMBL; AL162757; CAB85189.1; -.
SEQUENCE 1067 AA; 114012 MW; D3216DD7F4783B41 CRC64;
MEDLINE-98453137; PubMed-9781876;
Huguet E., Hahn K., Wengelnik K., Bonas
ThpaA mutants of Xanthomonas campestris
                                                                                                                                                                                                                                                                                                                                                            HRCS.
                                                                                                                            STRAIN=75-3
                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                Xanthomonas campestris (pv. vesicatoria).
Bacteria: Proteobacteria: gamma subdivision: Xanthomonas
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MEDLINE=20222556; PubMed=10761919;
MEDLINE=2022556; PubMed=10761919; PubMed=10761919; PubMed=10761919; PubMed=10761919; PubMed=10761919; PubMed=10761919; PubMed=10761919; PubM
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EMBL; AE002521; AAF42062.1; -.

TIGR; NMB1715; -.

SEQUENCE 1067 AA; 113973 MW;
                                                                                                                                                                                                                         NCBI_TaxID=341;
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Bacteria; Proteobacteria; beta subdivision;
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01-JUN-2000
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Ochiai H.; "Construction and characterization
                    SEQUENCE FROM N.A. STRAIN-MAFF 311018;
                                                                                                                                                                                                                                                                                            Mol. Plant Microbe Interact. 12:633-639(1999).
EMBL; AF160974; AAD46903.1; -
INTERPRO; IPR002191; -
PFAM; PF01313; Bac_export_3; 1.
PRINTS; PR00952; TYPE3IMQPROT.
                                                                Xanthomonas oryzae pv. ory
Bacteria; Proteobacteria;
                                                                                                 HRCS
                                                                                                                                                                                                                                                                                                                                         "A hrcU-homologous gene mutant of Xanthomonas campestris pv. 8ra that lost pathogenicity on the host plant but was able to the hypersensitive response on nonhosts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in pathogenicity but retain the ability to induce host-specific hypersensitive reaction.";
Mol. Microbiol. 29:1379-1390(1998).
EMBL; AF056246; AAD21322.1; -.
INTERPRO; IPR020191; -.
PFAM; PF01313; Bac_export_3; 1.
PFRINTS; PR00952; TYPE3IMQPROT.
                                                                                                                                                                                                                                                                                   SEQUENCE
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Oh C., Heu S., Yoo J.Y., Cho Y.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                               Xanthomonas campestris (pv. glycines).
Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                NCBI_TaxID=64187;
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Q9MCN5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Clustered hrp genes in Xanthomonas oryzae pv. Submitted (MAR-2000) to the EMBL/GenBank/DDBJ EMBL; AB045311; BAB07863.1; -. EMBL; AB040134; BAA92827.1; -. SEQUENCE 86 AA; 8944 MW; 3844AA65739BAD98
Hendrix R.W.; "Genomic sequences of bacteriophages HK97 and HK022: pervasive mosalcism in the lambdoid bacteriophages.";
                                                           SEQUENCE FROM N.A.
Juhala R., Ford M.E., Duda R.L., Youlton A., Hatfull G.F.,
                                                                                                                                     Bacteriophage HK022.
Viruses; dsDNA viruses,
Lambda phage group.
NCBI_TaxID=10742;
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Juhala R., Ford M.E., Duda R.L., Youlton A., Hatfull G.F.,
Hendrix R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteriophage HK97.
Viruses; dsDNA viruses,
Lambda phage group.
NCBI_TaxID=37554;
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Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
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Search completed: April 6, 2001, 01:28:06 Job time: 920 sec

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9b_est75:BE726886

9b_est11:AA749932

9b_est15:XM994265

9b_est16:A1084542

9b_est17:A1194189

9b_est17:A1194189

9b_est37:AV540058
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-Q-/cgn2_1/USP70_spco1/USQ9589870/runat_02042001_145246_15562/app_query.fasta_1.242
-DB=EST -OFMT=fastap -SUFFIX=rst -GAPOP=4.500 -GAPEXT=0.050
-MINNATCH=0.100 -LOOPEL=0.000 -LOOPEXT=0.000 -GAPOP=4.500
-QGAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=oligo-TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15
-DCCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15
-DCCALIGN=000-TOTFMT=pfs -NORM=ext -MINLEN=0 -MAXLEN=200000000
-USER=USQ9589870_@CGN1_1_2225 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXY
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gb_gss12:AQ823087
gb_gss21:AZ444910
gb_gss213:AQ936482
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A1973896
A1973896.1 GI:5770722
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A1973896 264 bp mrNA EST 17-JUL-2000 sd13d01.yl Gm-c1020 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1020-1562 5', similar to SW:CHEY_ECOLI P06143 CHEMOTAXIS PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  soybean.
Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-322 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Info@genomesystems.com web site: www.genomesystems.com Insert Length: 449 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primer: -40RP from Gibco.
Williams' plants that were greenhouse grown. The The CDNA library was prepared using the Stratagene phluescript II SK(+) library construction kit. First strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hem.methylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (v-A, C, or G) was added to the 3' end of the primer (GACAGACAGACAGACACTACTCTCGAC(T)18V) to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA polymerase and size-fractionated with a 400 bp cutoff, using a SizeSep 400 Spun column from Pharmacia. The column eluent was ligated to ECORI adaptors and phosphporylated. The XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500 bp cutoff, using GibcoBRL Life Technologies' cDNA Size Predigested
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1] ;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                          XhoI; This cDNA library was constructed from mRNA isolated from nodules on the roots of 2.5 month-old Glycine max 'Williams' plants that were greenhouse grown. The The cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="root nodules of greenhouse grown plants"
/lab_host="XL10-Gold"
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/clone_lib="Gm-c1020"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Glycine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                        http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 279 row: B column: 21
Seg primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                           library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Other_GSSs: RPCI-23-279B21.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., and and Fraser, C.M.
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                   BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      szhao@tigr.org
                                                                                                                                                  /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-279B21"
/clone_lib="RPCI-23"
/note-"Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size
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                                                                                                      /lab_host="DH10B"
                                                                                                                                   /sex="Female"
                                                                                                                                                                                                                                                                                                          location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bp DNA GSS 24-FEB-2000 RPCI-23 Mus musculus genomic clone RPCI-23-279B21
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LOCUS AQ836896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ836896 574 bp DNA GSS 30-AUG-1999 HS_5463_A1_H09_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1039 Col=17 Row=0, DNA sequence.
                                                                                                                                                                                                                                                                                              High quality sequence stop: 574.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu plate: 1039 row: O column: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                                                                  Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                      Seq primer: T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 574)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                    /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=1039 Col=17 Row=0"
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84 c 104 g 99 t
                                                                                                                                                    /clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
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Analyses of the Chlamydomonas reinhardtil Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants; project phase 2
Unpublished (2000)
Contact: Charles Hauser
DCMB Box 91000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST.
Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        894096B10.y2 C. reinhardtii CC-1690, Chlamydomonas reinhardtii cDNA, mRNA
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1 (bases 1 to 606)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: chauser@duke.edu
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                                                                                                                                                                                                                                   mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium billed with 5% CO2. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Stratagene) in the EcoRI (5') and XhOI (3') sites. PBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."
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1.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to
                                                                        9.00
1.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
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Percent Identity: 100.000
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National Inst. of Agri. Sci.
Suwon, Kyunggido, Korea
Tel: 82 331 290 0307
Fax: 82 331 290 0307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.

1 (bases 1 to 184)

Nahm, B. H., Kim, J. K., Cheong, J. J., Kim, S. I., Hahn, T. R. Moon, E. P., Kim, W. T., Kim, W. Y., Yang, M. S., Park, R. D., Sohn, U. I., Kang, K. Y., Lee, M. C. and Eun, M. Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
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/cultivar="Milyang23"
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                                                                                                  AI084542 258 bp mRNA
ov43d04.x1 Soares_testis_NHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM3-NN0030-110
500-178-f11&t3=2000-05-11&t4=1)
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
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                                      AI084542.1 GI:3422965
                                                                                 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue mRNA and cDNA amplification were performed under low stringency conditions." 53 c 39 g 69 t
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/dev_stage="Adult"
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AUTHORS
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                                                                                                                                                                                                                                                                                                    244 GGTTCCGGGACAGCACTGGGCTGG
                                                                                                                                                                                                                                                                                                                                         92 GlySerGlyThrAlaLeuGlyTrp 99
                                                                                                                                                                                                                                                            gb_est24:AI756574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 221.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G. E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: Robert_Strausberg@nih.gov cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 258)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                             EST.
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EtESTea02f10.yl Eimeria
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                                                                        Eimeria tenella
Liberator, P., Diaz, C., Tang, K., Marra, M.,
                                                                                          Eimeria tenella.
                                                                                                                             AI756574.1 GI:5150297
                                                                                                                                                   AI756574
                                                    Eukaryota; Alveolata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert Length:
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               (bases 1 to 299)
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                                                                                                                                                                  mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. " a 73 c 77 g 46 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1640071"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Soares_testis_NHT"
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Std
                                                    Apicomplexa; Coccidia;
                                                                                                                                                                                        mRNA
M5-6
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Hillier, L., Kucaba, T.,
                                                                                                                                                                                        18-JAN-2000
Eimeria tenella
                                                        Eimeriida;
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                                                          Eimeriidae;
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BASE COUNT
ORIGIN
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LOCUS AI194189
                                                                                                                                                                                                                                                                                                                                                                                             seq_name: gb_est17:AI194189
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                                                                                                                                                   ORGANISM
                                                     AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 AlaGinValSerAlaAlaGluAla 39
                                                                                                                                                                                                                                                                                                                                                                                                                                             GCACAGGTTTCTGCTGCTGAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Contact: David Sibley, Ph.D.
WashU-Merck Eimerla tenella project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Martin,J., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., SwallerT,Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Florence,N., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R., Wilson,R. and Sibley,D. WashU-Merck Eimeria tenella project
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 311)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
Contact David Sibley (toxoest@borcim.wustl.edu)
information relating to organism, libraries, or
Seq primer: -40Rp from Gibco
High quality sequence stop: 298.
                                                                                                                                                                                                                                                                                               ue81c04.rl Soares_NMPu
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                     mRNA sequence.
                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                             AI194189.1 GI:3745396
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                                                                                                                                                                            house mouse
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//lab_host="SOLR E. COl1"

//note="Vector: Bluescript SK-; Site_1: EcoRI; Site_2: XhoI

//note="Vector: Bluescript SK-; Site_1: EcoRI; May Synthesized from poly mRNA using containing a small percentage of host or bacterial containing a XhoI site. Following second strand synthesis, EcoRI adapters were ligated to the cDNA and products were size-selected on Sephacryl S500. cDNAs were digested with EcoRI/XhoI and cloned into lambda Zap II (Stratagene). Clones were converted to phagemids by mass excision using ExAssist helper phage and SOLR cells (Stratagene). Insert sizes range from 0.7-1.5
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1.000
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/db_xref="taxon:5802"
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COMMENT
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AUTHORS
TITLE
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ORIGIN
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     COMMENT
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seq_documentation_block:
LOCUS AV540058
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US-09-589-870-2 x AI194189
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ORGANISM
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                           AV540058 Arabidopsis thaliana cDNA clone RZ143h06F 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicinep Washington
DNA Res. 7, 175-180 (2000)
20363093
Contact: Erika Asamizu
                                                                          Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S. A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
                                                                                                                                                                                                 Arabidopsis thaliana Embryophyta; Tracheophyta; Spermatophyta; Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                      AV540058.1 GI:8701816
EST.
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                 thale cress.
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                                                                                                                                                                               (bases 1 to 326)
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h quality sequence stop: 213.
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Location/Qualifiers
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1.000
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/sex="female"
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/db_xref="taxon:10090"
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FEATURES

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FEATURES
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AUTHORS
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LOCUS BB059043
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                          , P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Kiyosawa, H., Kojima, Y., Kai, C., Sato, K., Shibata, K., Shibata, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tagawa, A., Shiraki, T., Tominaga, N., Toya, Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., RIKEN Mouse ESTs (Konno, H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
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Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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BB059043
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BB059043 RIKEN full-length enriched, 2 days
ganglion Mus musculus cDNA clone 7120486K15
Email: genome-res@rtc.riken.go.jp, uRL:http://genome.rtc.riken.go.jp/ uRL:http://genome.rtc.riken.go.jp/ Carninci.p., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki Carninci.p., Nuramatsu,M. and Hayashizaki,Y. Muramatsu,M. and Hayashizaki,Y. Thermostabilization and thermoactivation of thermolabile enzymes by
                                                                                                                                                                                                                                                           Genome Exploration Research Group, Life Science Tsukuba Center, Genome Science Laboratory
Genomical Institute of Physical and Chemical Research (RIKEN), Genomical Institute of Physical and Chemical Research (RIKEN),
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Tel: +81-298-36-9013
                                                                                                                                                                                                                                        Sciences Center
                                                                                                                                                Fax: +81-298-36-9098
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/tissue_type="roots"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
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/strain="Columbia"
/db_xref="taxon:3702"
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                                                                                                                                                                                                                                     Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
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                                                                                               z123a01.r1 Soares_pregnant_uterus_NbHPU IMAGE:502728 5', mRNA sequence.
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  Homo
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  sapiens
                                                                                                                                                                                                                                                                                                                          BB059043
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105 c 57 g 83 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sympathetic ganglion
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: Sall; 3' end: BamHI. Host: DH10B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="sympathetic ganglion"
/dev_stage="2 days neonate"
/lab_host="DH10B"
/note="Site_1: Sall; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="7120486K15"
/clone_lib="RIKEN_full-length_enriched, 2 days neonate
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/strain="C57BL/6J"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 374)

Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S., Traicoff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E.

Construction of a Characterized Clone Resource for Genomic
                                                                                                                                                                                                                                             B40058 374 bp DNA GSS 18-OCT-1997 HS-1050-B2-F08-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 772 Col=16 Row=L, DNA sequence.
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1 (bases 1 to 373)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.Hlnl.gov) for further information.
Seq primer: -28Mi3 rev2 from Amersham
High quality sequence stop: 295.
Location/Qualifiers
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Contact: Wilson RK
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                                                                                                                                     Homo sapiens
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Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5'
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/db_xref-"GDB:3807716"
/db_xref-"taxon:9606"
/clone-"IMAGE:502728"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gb_gss16:AZ131983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ131983 377 bp DNA GSS 02-JUN-2000 OSJNBb0111P08r CUGI Rice BAC Library (EcoRI) Oryza sativa genomic Clone OSJNBb0111P08r, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Mahairas GG, Zackrone KI
University of Washington
Seattle, WA 98195, USA
Tel: (206) 616-8744
Fax: (206) 685-7301
Email: kzackroneu washington.edu
                                                                    High quality sequence start: 14
High quality sequence stop: 363.
Location/Qualifiers
                                                                                                                         Email: rwing@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
                                                                                                                                                                                                                Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, U
                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.

1 (bases 1 to 377)
Wing,R.A. and Dean,R.A.
                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                    SSD
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                                                                                                                                                                                                                                                                    Contact: Wing RA
                                                                                                                                                                                                                                                                                      Unpublished (1998)
                                                                                                                                                                                                                                                                                                     A BAC End Sequencing Framework to Sequence the Rice Genome
                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa.
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                                                                                                                                                                             Tel: 864 656 7288 Fax: 864 656 4293
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/db_xref="taxon:9606"
/clone="plate=CT 772 Col=16 Row=L"
/clone_lib="CIT Human Genomic Sper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones
E-Coli DH10B"
                  /organism="Oryza sativa"
/strain="Japonica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="M"
/cultivar="Nipponbare"
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/clone\_lib="CUGI Rice BAC Library (ECORI)" /tissue\_type="Leaf" /lab\_host="E. coli DH10B"

/db\_xref="taxon:4530" /clone="OSJNBb0111P08r"

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REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
                                                     FEATURES
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US-09-589-870-2 x AZ131983/rev
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                     TITLE
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                    source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCACCGTGTCTATTACGGCAAGC 337
                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ur45c10.yl NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:3153234 5',
                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 390)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
BE553360
                                                                                                                                                                                                                                                                                                          Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE553360.1 GI:9817847
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                                                                                                                                       MGI:1055990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          house mouse.
                                                                                                             Seq primer: -40RP from Gibco
                                            quality sequence stop: :
Location/Qualifiers
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Rice is the most important food crop in the world. Half of
the world population, especially those inhabiting highly
populated areas of the humid tropics and subtropics, rely
on rice as their primary source of carbohydrate.
Monocotyledonous rice is a diploid plant (2n=24) with a
haploid genome equivalent of 431 Mbp (Arumuganathan and
Earle, 1991). The relatively small genome of rice, three
times larger than that of Arabidopsis, makes it suitable
for genomic studies. In order to facilitate positional
cloning, physical mapping and genome sequencing of rice,
we have constructed a HAC library from Oryza sativa,
Nipponbare variety using EcoRI as the cloning enzyme. The
library contains 55,296 clones with an average insert size
of 121 Kb providing approximatley 15 haploid genome
equivalents. The deep coverage allows the isolation a
particular sequence with a probability of 99.9 %. Three
high density filters, each containing 18,432 clones
(doubly spotted), represent the whole library for colony
screening and can be requested from the Clemson University
BAC/EST Resource Center (www.genome.clemson.edu)."
87 a 136 t 1 others
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/organism="Mus musculus"
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SOURCE

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alignment_block:
US-09-589-870-2 x BE553360
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12 SerLeuThrThrValSerIleThr 19
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                                                                 to: BE553360
                                                                                                                                                                                                                                                                                 110
                                                                                                                                                                                                                                                                         /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="NCI_CGAP_Mam2"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
                                                                                                                                                                       8.00
1.000
                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:3153234"
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                                                                   from: 1
                                                                                                                                      Gaps: 0
Percent Identity: 100.000
                                                                     to: 390
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Result
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                  Score
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seq length: 2000000000
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Y84020
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Y80513
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Y44701
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21.7	69.4	69.4	٠	70.5	•	72.1	72.1	•	72.5		•	•	•	•	•	87.4	87.6	•	87.8	•	•	88.5		•	•	•	89.2	•	•	•	96.3	•
40	122	122	140	685	402	128	128	128	673	168	270	415	159	159	159	159	159	159	159	159	159	159	159	159	160	163	162	161	435	186	186	183
œ	21	21	17	17	15	18	17	14	17	21	20	15	18	18	18	18	18	18	18	18	18	18	18	18	10	9	21	21	15	21	21	19
P70491	Y80517	Y80516	W04210	W04209	R56485	W29308	W04211	R34722	W04208	Y44700	Y28928	R56484	W29320	W29317	W29318	W29319	W29312	W29315	W29316	W29313	W29314	W29309	W29311		P93531	P80160			R56483	11 Y84022	Y84021	W59218
quenc	treptomyces avid	omyces avid	Mutant Streptomyce	t streptavid	0 and	Core-		Core streptavidin.	Streptavidin/lucif	o proteinas	rotei	pRAS109												Streptavidin prote	ರ	prote	Streptomyces avidi	avid	pRAS10	acid	mino acid sequen	S. avidinii strept

## ALIGNMENTS

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RESULT
P60625
                     DNA sequences and hybrid DNA sequences - streptavidin-like polypeptide, also join e.g. tissue plasminogen activator
                                                         WPI; 1986-106643/16.
N-PSDB; N60626.
                                                                                                                                                                                       Streptomyces
                                                                                                                                                                                                         Antibiotic; biotin binding affinity; fusion protein
                                                                                                                                                                                                                         Sequence of a streptavidin-like polypeptide encoded by SA307
                                                                                                                                                                                                                                           13-AUG-1991
                                                                                  Meade HM,
                                                                                                                     02-OCT-1984;
                                                                                                                                     01-OCT-1985;
                                                                                                                                                       10-APR-1986.
                                                                                                                                                                       WO8602077-A.
                                                                                                                                                                                                                                                              P60625;
                                                                                                                                                                                                                                                                             P60625 standard; Protein; 183 AA
                                                                                                    (MEAD/) MEADE H M.
                                                                                  Garwin JL,
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                                                                                                                     84US-0656873
                                                                                                                                     85WO-0001901.
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joined to another protein,
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Disclosure; Fig.

2; 54pp; English

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
Streptavidin is a 60kD protein isolated from Streptomyces avidinii binds extremely tightly to the vitamin biotin. It is composed of form
                                                                                                       Fig 1; page 1/5; 22pp; English
                                                                                                                                                       biotin-binding activity
                                                                                                                                                                                 DNA sequence encoding streptavidin and vector - comprising hybrid gene encoding fusion protein
                                                                                                                                                                                                                                                        WPI; 1989-130040/17.
                                                                                                                                                                                                                                                                                                          Edwards RM
                                                                                                                                                                                                                                                                                                                                                                                                        08-OCT-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W08903422-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces avidinii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptavidin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The inventors claim the DNA sequence in SA307 which codes for a steptavidin-like polypeptide (see N66026), and the polypeptide encoded by it (P60625). They also claim hybrid SQs comprising N60626 and a second sequence coding for another protein, polypeptide, peptide or AA (pref. tissue plasminogen activator (TPA)).
                                                                                                                                                                                                                                                                                                                                                        (BRBI-) BRIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-APR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptavidin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P93530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P93530 standard; protein; 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      galtgtyesavgnaesryvltgrydsapatdgsgtalgwtvawknnyrnahsattwsgqy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vqq 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                        BIO-TECHN LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces avidinii; biotin.
                                                                                                                                                                                                                                                                                                                                                                                                          87GB-0023661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ĀĀ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     88WO-GB00831.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="This sequence was as the basis for the design
for the synthetic gene of the present invention."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25..159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Leader sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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Pred. No. 2.5e-76;
; Mismatches 0;
                                                                                                                                                                                 protein with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 183;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
Streptavidin prodn. from Bacillus subtilis - using signal protein from bacterial exo-protein and expression element from Gram
                                  P-PSDB;
                                                                 Nagarajan
                                                                                                             29-MAY-1992;
                                                                                                                                   27-MAY-1993;
                                                                                                                                                         09-DEC-1993
                                                                                                                                                                            W09324631-A
                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                     Streptomyces avidinii.
                                                                                                                                                                                                                                                                                                                         Streptavidin; protein secretion; Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                Streptavidin
                                                                                                                                                                                                                                                                                                                                                                                             R44491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    identical subunits of 15kD and binds 4 mole of biotin per mole of protein. It is structurally related to the protein avidin. It can be readily conjugated to a range of other proteins. In order to facilitate the incorporated of streptavidin into expression vectors and the production of novel chimeric proteins containing streptavidin functionality, an improved novel synthetic gene for streptavidin has been constructed (n90755) based on the amino acid sequence of mature
                                                                                      (DUPO ) DU PONT DE NEMOURS &
                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                      27-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                  R44491 standard; Protein; 183 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              streptavidin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
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                                 1993-405822/50.
DB; Q53412.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vqq 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GALTGTYESAVGNAESRYVLIGRYDSAPATDGSGTALGWTVAWKNNYRNAHSATTWSGQY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VQQ 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          galtgtyesavgnaesryvltgrydsapatdgsgtalgwtvawknnyrnahsattwsgqy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 AA;
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                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                             92US-0891524
                                                                                                                                   93WO-US05240
                                                                                                                                                                                                              /label= streptavidin 37..183
                                                                                                                                                                                                                                                          1..24
                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                    25..183
                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                            'label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                 "expressed by transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                       G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 936; DB 10;
Pred. No. 2.5e-76;
; Mismatches 0;
                                                                                       H
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                                                                                                                                                                                                  B. subtilis"
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Best Local Similarity
Matches 183; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 1b; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptavidin; biotin; anti-interference reagent; detection; mutein; avidin; non-specific binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wild-type streptavidin protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence
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Disclosure; Page 17-18; 26pp; German
                                                                           Streptavidin and avidin muteins with reduced binding affinity for biotin - useful for reducing interference from nonspecific binding
                                                                                                                                                          WPI; 1997-482043/45
N-PSDB; T73193.
                                                                                                                                                                                                                                                              Brandstetter H,
                                                                                                                                                                                                                                                                                                                                                                  01-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-OCT-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DE19637718-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                      in assays
                                                                                                                                                                                                                                                                                                                                                                                                                     16-SEP-1996;
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                                                                                                                                                                                                                                                                                                              (BOEF ) BOEHRINGER MANNHEIM GMBH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VGGAEARINTQWLLTSGTTEANAWKSTLVGHDTFTKVKPSAASIDAAKKAGVNNGNPLDA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                     96DE-1013053
                                                                                                                                                                                                                                                                                                                                                                                                                     96DE-1037718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label- signal 25..183
                                                                                                                                                                                                                                                           Deger A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                           Engh R,
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                                                                                                                                                                                                                                                                Kopetzki E,
                                                                                                                                                                                                                                                                Mueller
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RESULT W59216
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Best Local Similarity
Matches 183; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptavidin; ligand; binding affinity; mutant; isolation; purification; recover; immobilise.
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Streptavidin mutants with higher binding affinity for peptide ligands - have mutation in amino acid region 44-53, used to isolate,
                                                                                            N-PSDB; V34714.
                                                                                                                          WPI; 1998-218868/20
                                                                                                                                                                                                                                                                                                                                                                                     09-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces avidinii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S. avidinii streptavidin protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W59216 standard; Protein; 183
                                                                                                                                                                                                                                                        (BIOA-) INST BIOANALYTIK GMBH GOETTINGEN
                                                                                                                                                                                                                                                                                                                       10-OCT-1996;
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RESULT Y17868 ID 7818 
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Best Local
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                              N-PSDB; X80198
                                                                                                                    Cederholm-Williams SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Avidin; streptavidin; batroxobin; fibrinogen converting enzyme; hybrid; fusion protein; sealant; surgery; reduce bleeding; fibr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus streptavidin.
                                                          WPI; 1999-385599/32.
                                                                                                                                                                           (BRIM ) BRISTOL-MYERS SQUIBB CO
                                                                                                                                                                                                                                         09-DEC-1997;
                                                                                                                                                                                                                                                                                                09-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-AUG-1999
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      groups, the C-terminal carboxy groups or side-chain functionalities; (ii) via a bifunctional linkage moiety linking the groups or functionalities; or (iii) by the first member binding to the second member of the binding pair, where the second member of the binding pair is covalently attached to the first polypeptide chain. The FCE can be used in a method for producing fibrin. Fibrin is useful as a sealant in surgery to, e.g. reduce bleeding by sealing blood vessels, and tissues that have been dissected either in surgery or through wounding. The fusion protein allows for the removal of the fibrinogen converting enzyme from the fibrin sealant preparation via the binding of streptavidin to a biotin solid support. The present sequence represents Streptococcus streptavidin as given in the present invention.
15-JUL-1998;
                              15-JUL-1999;
                                                                                              WO200004049-A1
                                                                                                                                                Peptide
                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                          Potato proteinase inhibitor-II; PPI-II; streptavidin; worm; insect; plant-noxious protein; pest resistance; moth; insect; weevil; grub; beetle; fly; thrip; locust; cricket; borer; mite; looper;
                                                                                                                                                                                                                                                                                                             Streptavidin protein for recombinant pART27 vector.
                                                                                                                                                                                                                                                                                                                                                                                Y44701;
                                                                                                                                                                                                                                                                                                                                                                                                               Y44701 standard; Protein; 183 AA.
                                                                                                                                                                                                                                                                                                                                              25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 28; 35pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          {\tt 1} \ {\tt mrkivvaaiavsIttvsitasasadpskdskaqvsaaeagitgtwynqlgstfivtagad}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention describes a fibrinogen-converting enzyme fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GALTGTYESAVGNAESRYVLTGRYDSAPATDGSGTALGWTVAWKNNYRNAHSATTWSGQY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                              (first entry)
98NZ-0331002
                                99WO-NZ00110.
                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 936; DB 20; 100.0%; Pred. No. 2.5e-76; ... Mismatches 0;
                                                                                                                              "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
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is linked to
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Best Local
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Transformation of plant genome with the vector can produce pest resistance in plants, plant derived products and stored harvest material. Pests that can be controlled include, cotton bollworm, tropical army-worm, European corn-borer or red mite, tobacco horn worm, loopers, rice stem borer, porina, cutworms, diamondback moth, potato tuber moth, codling moth, Indian meal moth, gypsy moth, argentine stem weevil, clover root weevil, grass-grubs, corn rootworm, rice and wheat weevils, mealworms, flour beetles, black field cricket, locusts, sawfiles, Western flower thrips, Hessian flies or two-spotted mite.
30-JUL-1999;
                            17-FEB-2000
                                                        WO200007427-A2
                                                                                  Streptomyces avidinii.
                                                                                                                         Plant somatic tissue degeneration; plant essential factor; depletion; viability; sps gene; plant development; plant morphology; flower;
                                                                                                                                                                     Streptomyces
                                                                                                                                                                                                 06-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 12; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New chimeric polypeptide and composition comprising useful for conferring pest resistance on plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-171244/15
N-PSDB; Z49867.
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                                                                                                                                                                                                                                                      Y80512 standard; Protein; 186 AA
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                                                                                                             plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 AA;
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ilarity 100.0%;
Conservative (
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99WO-IL00420.
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Pred. No. 2.5e-76;
); Mismatches 0;
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Best Local
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                                                                               Plant somatic tissue degeneration; plant essential factor; viability; mst gene; plant development; plant morphology; fruit plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Degeneration of somatic plant tissue by expression of a heterologous protein, useful for controlling plant development and morphology, such as decreasing the number of flowers present to increase the number of
                                                      Streptomyces avidinii.
                                                                                                                                      Streptomyces avidinii mst protein.
                                                                                                                                                                                               Y80513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                           WO200007427-A2
                                                                                                                                                                  06-JUN-2000
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                                                                                                                                                                                                                          Y80513 standard; Protein; 184 AA.
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                                                                                                                                                                                                                                                                                                                       VQQ 183
                                                                                                                                                                                                                                                                                                                                                                                                        galtgtyesavgnaesryvltgrydsapatdgsgtalgwtvawknnyrnahsattwsgqy
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                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 936; DB 21;
Pred. No. 2.5e-76;
Mismatches 0;
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Matches 182;
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27-AUG-1987
                                                              Streptomyces
                                                                                                                                                 06-MAR-1991 (first entry
                                   WO8705026-A
                                                                                          Streptavidin; N-terminal;
                                                                                                                        Streptavidin sequence
                                                                                                                                                                                                             P70492 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Examples; Page 85; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kapulnik Y, Ginzberg I;
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                                                                                            fusion
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                                                                                            gene;
                                                                                          fusion protein;
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Best Local S
Matches 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence is that of streptavidin from S.avidinii. Streptavidin may be expressed from a fusion gene comprising its coding gene and encoding a target protein of interes, where he streptavidin has binding sites for biotin or deriv. The streptavidin has 4 binding sites free for biotin, and is produced free of biotin contamination. Improved streptavidins may also be produced by site-directed mutagenesis. The fused gene may be used to produce labelled, chemically-modified proteins in vivo, and to isolate
                                                                               Streptomyces
                                                                                                                        Streptavidin; monomer; biotin binding domain; functional domain; biotin; cell adhesion peptide; adaptor; streptavidin/biotin interaction;
                                                                                                                                                                  Amino acid sequence of the wildtype streptavidin monomer
                                                                                                                                                                                             03-JUL-2000
                                                                                                                                                                                                                         Y84020;
                                                                                                                                                                                                                                                    Y84020 standard; protein; 183 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contamination. Improved streptavidins may also be pr
site-directed mutagenesis. The fused gene may be use
labelled, chemically-modified proteins in vivo, and t
proteins when only the sequence of the gene is known.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                            vascular device;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Axel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                 avidinii
                                                                                                                                                                                             (first entry)
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                                                    Location/Qualifiers
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99.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 928; DB 8; Le
Pred. No. 1.3e-75;
Prematches 0;
                                                                                                         prosthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 182;
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WO200011152-A1

/note=

"propeptide'

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Best Local Similarity
Matches 182; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        biotin and also have another function, for e.g. binding to a cell through the secondary functional domain comprising a cell adhesion peptide. The streptavidin molecules are useful as adaptors to bring, via a streptavidin/biotin interaction, the secondary functional domain into proximity with a cell or molecule to be affected and as a coating for substrates such as vascular devices or prostheses. Therefore, any compound of interest, such as a nucleic acid, protein, peptide, organic compound, inorganic compound, polysaccharide or a combination, can be targeted, delivered or immobilized using them. The molecules, when comprising an antibody for its secondary functional domain, are also useful in diagnostic applications for detecting analytes.
                                Streptavidin; ligand; binding affinity; mutant; isolation; purification; recover; immobilise.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a wildtype streptavidin monomer. The specification describes streptavidin molecules comprising a biotin binding domain and a secondary functional domain. The molecules are adaptors with inherent effector function. They can therefore, bind to adaptors with inherent effector function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mutant streptavidin molecule, useful as an adaptor and a coating for substrates such as vascular devices or prostheses, comprises a biotin binding domain and a secondary functional domain -
   Streptomyces avidinii
                                                                                                                 27-AUG-1998
                                                                                                                                                W59217;
                                                                                                                                                                                W59217 standard; Protein; 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                               avidinii streptavidin mutant protein
                                                                                                                                                                                                                                                                                 VQQ 183
                                                                                                                                                                                                                                                            vgq 183
                                                                                                                                                                                                                                                                                                                                                                                          vggaearintqwlltsgtteanawkstlvehdtftkvkpsaasidaakkagvnngnplda
                                                                                                                                                                                                                                                                                                                                           VGGAEARINTQWLLTSGTTEANAWKSTLVGHDTFTKVKPSAASIDAAKKAGVNNGNPLDA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                            mrkivvaaiavslttvsitasasadpskdskaqvsaaeagitgtwynqlgstfivtagad 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MRKIVVAAIAVSLTTVSITASASADPSKDSKAQVSAAEAGITGTWYNQLGSTFIVTAGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 35-36; 43pp; English
                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McDevitt TC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3
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99.5%;
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Pred. No. 1.3e-75;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 183;
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RESULT W59218 ID W5

13

W59218 standard; Protein; 183

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a mutant streptavidin protein isolated from CC Streptomyces avidinii where the residues ESAV at position 44-47 of the mature wild type sequence are replaced by VTAR. This sequence is CC used to produce mutants which are used in a method to assay the binding affinity of streptavidin mutants. These mutants have a mutation within CC the amino acid (aa) region 44-53 of the wild-type protein show a higher CC the sequence of formula Trp-X-His-Pro-Gln-Phe-Y-Z where X = any aa; Y CC and Z are both Gly, or Y = Glu and Z = Arg or Lys. Recombinant CC streptavidin mutants can be used to isolate, purify and determine CC proteins or to determine/recover substances that contain CC streptavidin-binding groups. Such compounds may also be used to CC immobilise fusions on microtitre plates, microbeads or sensor chips. NOTE: This sequence does not appear in the specification but has the value of t
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptavidin mutants with higher binding affinity for peptide ligands - have mutation in amino acid region 44-53, used to isolate, purify or determine fusion proteins including these ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page -; 21pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BIOA-) INST BIOANALYTIK GMBH GOETTINGEN.
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                                                                                                                                                                                                                                                                                                                 1 MRKIYVAAIAVSLTTVSITASASADPSKDSKAQVSAAEAGITGTWYNQLGSTFIVTAGAD
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DB; V34715.
                                                                                                                                                                            galtgtyvtargnaesryvltgrydsapatdgsgtalgwtvawknnyrnahsattwsgqy
                                                                                                                                                                                                  GALTGTYESAVGNAESRYVLTGRYDSAPATDGSGTALGWTVAWKNNYRNAHSATTWSGQY 120
                                                                                                                                                                                                                                                                                                                                                                 180;
                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                          183
183
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/label= VTAR68ESAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Wild type ESAV is replaced by VTAR. Numbering
is from the start of the mature protein"
                                                                                                                                                                                                                                                                                                                                                                                    98.2%;
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                                                                                                                                                                                                                                                                                                                                                              Score 919; DB 19;
Pred. No. 8.2e-75;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                         Length 183;
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Matches
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                                                                                                                                                                                                                                                                                      affinity of streptavidin mutants. These mutants have a mutation within the amino acid (aa) region 44-53 of the wild-type protein show a higher binding affinity than the wild-type for peptide ligands that include the sequence of formula Trp-X-His-Pro-Gln-Phe-Y-Z where X = any aa; Y and Z are both Gly, or Y = Glu and Z = Arg or Lys. Recombinant streptavidin mutants can be used to isolate purify and determine proteins or to determine/recover substances that contain streptavidin-binding groups. Such compounds may also be used to immobilise fusions on microtitre plates, microbeads or sensor chips. NOTE: This sequence does not appear in the specification but has been constructed from the wild-type streptavidin sequence represented in V24714.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a mutant streptavidin protein isolated from Streptomyces avidinii where the residues ESAV at position 44-47 of the mature wild type sequence are replaced by IGAR. This sequence is used to produce mutants which are used in a method to assay the binding
                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page -; 21pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptavidin mutants with higher binding affinity for peptide ligands - have mutation in amino acid region 44-53, used to isolate, purify or determine fusion proteins including these ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers Misc-difference 68..71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptavidin; purification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Skerra A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces avidinii. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S. avidinii streptavidin mutant protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BIOA-) INST BIOANALYTIK GMBH GOETTINGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-APR-1998
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 121
                                 61
                                                                61
                                                                                                                                                                                 Local Similarity
                                                                                                                                \vdash
VGGAEARINTQWLLTSGTTEANAWKSTLVGHDTFTKVKPSAASIDAAKKAGVNNGNPLDA 180
                                                GALTGTYESAVGNAESRYVLTGRYDSAPATDGSGTALGWTVAWKNNYRNAHSATTWSGQY 120
                                                                                                                                MRKIVVAAIAVSLTTVSITASASADPSKDSKAQVSAAEAGITGTWYNQLGSTFIVTAGAD
                              galtgtyigargnaesryvltgrydsapatdgsgtalgwtvawknnyrnahsattwsgqy 120
                                                                                            mrkivvaaiavslttvsitasasadpskdskaqvsaaeagitgtwynglgstfivtagad 60
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                                                                                                               Voss S;
                                                                                                                                                                                                                                               183 AA;
                                                                                                                                                                Conservative
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recover; immobilise.
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is from the start of the mature protein"
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                                                                                                                                                                               98.0%;
98.4%;
                                                                                                                                                                0;
                                                                                                                                                                            Score 917; DB 19;
Pred. No. 1.2e-74;
                                                                                                                                                                Mismatches
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                                                                                                                                                                                            Length 183;
                                                                                                                                                                Indels
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                                                                                                                                                            Gaps
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RESULT ID AND SERVING 
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                                                             for substrates such as vascular devices or prostheses. Therefore, any compound of interest, such as a nucleic acid, protein, peptide, organic compound, inorganic compound, polysaccharide or a combination, can be targeted, delivered or immobilized using them. The molecules, when comprising an antibody for its secondary functional domain, are also useful in diagnostic applications for detecting analytes.
                                                                                                                                                                                                                                                              adaptors with inherent effector function. They can therefore, bind to biotin and also have another function, for e.g. binding to a cell through the secondary functional domain comprising a cell adhesion peptide. The streptavidin molecules are useful as adaptors to bring, via a streptavidin/biotin interaction, the secondary functional domain into proximity with a cell or molecule to be affected and as a coating
      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   streptavidin. It is a streptavidin molecule of the invention. The specification describes streptavidin molecules comprising a biotin binding domain and a secondary functional domain. The molecules are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mutant streptavidin molecule, useful as an adaptor and a coating for substrates such as vascular devices or prostheses, comprises a biotin binding domain and a secondary functional domain -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; Page 36-37; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-224689/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptavidin; monomer; biotin binding domain; functional domain; biotin; cell adhesion peptide; adaptor; streptavidin/biotin interaction; substrate; vascular device; prosthesis; fibrinonectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a fusion of fibrinonectin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y84021;
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Matches 179; Best Local Similarity

Conservative

96.3%; 96.2%;

Score 901.5; DB 21; Pred. No. 3e-73; Mismatches

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The present sequence represents a fusion of osteopontin and construction. It is a streptavidin molecule of the invention. The specification describes streptavidin molecules comprising a biotin compound; and describes streptavidin molecules comprising a biotin compound; with inherent effector functional domain. The molecules are damptors with inherent effector function, for e.g. binding to a cell compound; the secondary functional domain comprising a cell adhesion peptide. The streptavidin molecules are useful as adaptors to bring, compound; a streptavidin/biotin interaction, the secondary functional domain comprising a cell adhesion compound; a streptavidin/biotin interaction, the secondary functional domain compound; incorporates such as vascular devices or prostheses. Therefore, any compound, incorporate compound, polysaccharide or a combination, can be targeted, delivered or immobilized using them. The molecules, when compound, an antibody for its secondary functional domain, are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mutant streptavidin molecule, useful as an adaptor and a coating for substrates such as vascular devices or prostheses, comprises a biotin binding domain and a secondary functional domain -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptavidin; monomer; biotin binding domain; functional domain; biotin; cell adhesion peptide; adaptor; streptavidin/biotin interaction; substrate; vascular device; prosthesis; osteopontin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 38; 43pp; English.
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Best Local S
Matches 179
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                                                                                                                                   Local Similarity 96.: les 179; Conservative
                                                                                                 ldavqq 186
                 LDAVQQ
                                                                          GALTGTYESAVGNAESRYVLTGRYDSAPA---TDGSGTALGWTVAWKNNYRNAHSATTWS
                                                                 galtgtyesavgnaesryvltgrydsapgrgdsvgsgtalgwtvawknnyrnahsattws
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                                                                                                                                           96.1%;
96.2%;
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Pred. No. 4.6e
1; Mismatches
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Search completed: April 6, 2001, 00:15:59 Job time: 15499 sec

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gb_ba1:ACEG1PSEU
gb_ba2:MCU61725
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gb_pat1:A93663
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gb_sy:ASY14583
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Query: US-09-589-870-2
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gb_sy:AGSTREP
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Database length: -1736092196
Search time (sec): 926.690000
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-Q-/cgn2_1/USPTO_spool/US9589870/runat_02042001_145219_15081/app_query.fasta_1.242
-DB-GenEmbl -QFWF_fastap -SUFFIX-rige -GAPOP=12.000 -GAPEXT=4.000
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-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.000 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -XGAPEXT=0.500 -DELEXT=7.000 -START=1 -MATRIX=bLosum62 -TRANS=human40.cd1
-LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTENT=pfs -NORM=ext -MINLEN=0
-MAXLEN=20000000000 -USER=US9589870_@CGN1_1_4349 -NCPU=6
-ICPU=3 -LONGLOG -NO_XLPXY -WAIT -THREADS=1
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| A93663 Sequence 15 from Patent |
| 117472 Sequence 1 from patent |
| 117472 Sequence 1 from patent |
| 120170 DNA encoding mutated st |
| 1413390 Oligonucleotide probe (48 |
| 1413391 Oligonucleotide probe (47 |
| 1413391 Oligonucleotide probe (47 |
| 143391 Sequence 3 from Patent |
| 1430691 Sequence 1 from Patent |
| 1430691 Strongylocentrotus purp |
| 163861 Sea urchin fibropellin |
| 163861 Sea urchin fibropellin |
| 167389 Escherichia coli (clone |
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                      Z48958 A.caulinodans egl pseud
U61725 Moraxella catarrhalis
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gb_pr1:AB023048
gb_pr5:AP000511
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seq_documentation_block:
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Ratio: 5.115
Percent Similarity: 100.000
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                                                                                                       17 rIleThrAlaSerAlaSerAlaAspProSerLysAspSerLysAlaGlnV
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rGluSerAlaValGlyAsnAlaGluSerArgTyrValLeuThrGlyArgT
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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Argarana,C.E., Kuntz,I.D., Birken,S., Axel,R. and Cantor,C.R.
Molecular cloning and nucleotide sequence of the streptavidin gene
Nucleic Acids Res. 14 (4), 1871-1882 (1986)
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US-09-589-870-2 x A93649
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LOCUS A93649
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Mueller,R.D. and Deger,A.D.
Recombinant inactive core streptavidin mutants
Patent: EP 079990-A 08-OCT-1997;
BOEHRINGER MANNHEIM GMBH (DE)
LOCATION/Qualifiers
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Align seg 1/1

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                                             alignment_scores:
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Quality: 933.00
Ratio: 5.098
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Sequence 2 from Patent US 48
101349
101349.1 GI:270134
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Cantor.C.R., Axel.R. and Argarana.C.

DNA encoding streptavidin, streptavidin produced therefrom, polypeptides which include amino acid sequences present in streptavidin and uses thereof patent: US 4839293-A 2 13-JUN-1989;
                                                                                                                                                                                  The
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GenBank staff at the national from the entry [NCBI glbbsq 169185] from the This sequence comes from Fig. 4.

Location/Qualifiers

1. .625
                                                                                                                             Streptomyces violaceus Tu 2460.
Streptomyces violaceus
Streptomyces violaceus
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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1 (bases 1 to 625)
Bayer,E.A., Kulik,T., Adar,R. and Wilchek,M.
Close similarity among streptavidin-like, biotin-binding
                                                                                                                                                                                                           S78777
                                                                  from Streptomyces
Blochim. Blophys. Acta 1263 (1),
                                                               95359204
                                                                                                                          Actinomycetales; Streptomycineae;
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Genomic, 62
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alignment_block:
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wynqlcstfivtagadcaltgtyesavcnaeskyvltgrydsapatdgsgtalgwtva
wknnyrnahsattwsggyvggtearintowlltsgtteanawkstlvghdtftkvkps
aasidaakkagvnnghpldavoq"
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/protein_id="AAB35015.1"
/db_xref="GI:1042194"
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/db_xref="taxon:1936"
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                                                 rGluSerAlaValGlyAsnAlaGluSerArgTyrValLeuThrGlyArgT 84
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Streptomyces violaceus
Bacteria; Actinobacteriae;
Bacteria; Streptomycineae; Streptomycetaceae; St
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Bayer,E.A., Kulik,T., Adar,R. and Wilchek,M.
Close similarity among streptavidin-like, biotin-binding proteins
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Location/Qualifiers
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WKNNYRNAHSATTWSGQYVAGSEARINTQWLLTSGTTAANAWKSTLVGHDTFTKVKPS
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/db_xref="taxon:1936"
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                   Quality:
Ratio:
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IMP CANCER RES TECH (GB)
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Location/Qualifiers
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alignment\_block:  $US-09-589-870-2 \times A39565$ 

Align seg 1/1 to: A39565

from: 1

to: 1356

20 AlaSerAlaSerAlaAspProSerLysAspSerLysAlaGlnValSerAl

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Compounds for targeting
Patent: EP 0815872-A 07-JAN-1998;
IMP CANCER RES TECH (GB)
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LOCUS AR082490
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Ratio:
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AR082490
AR082490.1 GI:1
                                               Epenetos, A. Antoniou, Spooner, R. Anth
Compounds for targeting
Patent: US 5973116-A 4 26-OCT-1999;
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LOCUS A20698
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                                                          CARRIER-BOUND RECOMBINANT PROTEIN, PROCESS USE AS AN IMMUNOGEN AND VACCINE Patent: WO 9113155 A 2 05-SEP-1991; Location/Qualifiers
                                                                                                                        synthetic construct artificial sequence.
1 (bases 1 to 525)
                                                                                                                                                               synthetic construct.
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Lubitz,W. and Szostak,M.P.
Lubitz,W. and Szostak,M.P.
Liminogens comprising the non-lytic bacteriophages MS2 or PhiX174
Patent: US 5470573-A 2 28-NOV-1995;
                                                                                                                                          Sequence 2 from patent I15647
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1 (bases 1 to 498) Huston, J.S. and Opp
                                  Unknown
                                                                           Sequence 38 from Patent 109059
                     Unclassified
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                                                                  I09059.1 GI:588242
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                                                                   Sequence 7 from Patent W09728263
A93838
unclassified
              unidentified unidentified
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REFERENCE AUTHORS TITLE

1 (bases 1 to 498) Lubitz, W. and Sleytr, U. RECOMBINANT EXPRESSION OF

S-LAYER PROTEINS

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SOURCE
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                                                                                                                       DEFINITION
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US-09-589-870-2 x A93838
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Ratio: 5.245
Percent Similarity: 100.000
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                                              ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                       pGlySerGlyThrAlaLeuGlyTrpThrValAlaTrpLysAsnAsnTyrA 108
                                                                                                                                                                                                                          GlyAsnProLeuAspAlaValGlnGln 183
                                                                                                                                                                                                            GGTAACCCTCTAGACGCTGTTCAGCAA 483
                                                                                                                                                                                                                                                                    AGCCTTCTGCTGCTAGCATTGATGCTGCCAAGAAAGCAGGCGTAAACAAC
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                                                                                                                                                                                                                                                                                                                               GAATGCATGGAAATCGACACTAGTAGGTCATGACACCTTTACCAAAGTTA 406
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Streptomyces avidinii.
Streptomyces avidinii
Streptomyces avidinii
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
1 (bases 1 to 507)
                                                                                                   507 bp
S.avidinii synthetic
A00743
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LUBITZ WERNER (AT): SLE1:..
Location/Qualifiers
/98
                                                                                         A00743.1 GI:14605
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137 c 131 g
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Gaps:
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alignment_block:
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Ratio: 5.245
Percent Similarity: 100.000
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TITLE
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                                                                                                             aAsnAlaTrpLysSerThrLeuValGlyHisAspThrPheThrLysValL
                                                                                                                                                                    GluAlaArgIleAsnThrGlnTrpLeuLeuThrSerGlyThrThrGluAl
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                                                                                              GAATGCATGGAAATCGACACTAGTAGGTCATGACACCTTTACCAAAGTTA
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                                         AGCCTTCTGCTAGCATTGATGCTGCCAAGAAAGCAGGCGTAAACAAC
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SYNTHETIC GENE
SYNTHETIC GENE
Patent: WO 8903422-A 2 20-APR-1989;
British Bio-Technology Ltd
British Bio-Technology Ltd
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/translation="MDPSKDSKAQVSAAEAGITGTWYNWKNNYRNAHSATTWSGQYVGGAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARINTQWLLTSGTTEANAWKSTLVGHDTFTKVKPSAASIDAAKKAGVNNGNPLDAVQQ
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/db_xref="taxon:1895"
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COMMENT
FEATURES
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AUTHORS
TITLE
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ORGANISM
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US-09-589-870-2 x A00744/rev
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ORIGIN
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Ratio: 5.245
Percent Similarity: 100.000
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                                             158 ysProSerAlaAlaSerIleAspAlaAlaLysLysAlaGlyValAsnAsn
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                                                                                                                                                  GAGGCTCGTATCAACACTCAGTGGCTGTTAACATCCGGCACTACCGAAGC
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                             AGCCTTCTGCTAGCATTGATGCTGCCAAGAAAGCAGGCGTAAACAAC
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Streptomyces avidinii.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; St
1 (bases 1 to 507)
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/db_xref="taxon:1895"
130 c 137 g 125 +
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streptavidin.
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Seq_documentation_block:
LOCUS
A39567
DEFINITION Sequence 6 frc
ACCESSION A39567
VERSION A39567.1 GI:2
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AUTHORS
TITLE
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US-09-589-870-2 x A39567
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                                                               1053 TGCACCTGCCACCGATGGCTCTGGTACCGCTCTGGGCTGGACTGTGGCTT 1102
                                                                                                                                              1003 GCGGTTGGTAACGCAGAATCCCGCTACGTACTGACTGGCCGTTATGACTC
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                                                                                                                                                                 70 AlaValGlyAsnAlaGluSerArgTyrValLeuThrGlyArgTyrAspSe
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                                                                                rAlaProAlaThrAspGlySerGlyThrAlaLeuGlyTrpThrValAlaT 103
                                                                                                                                                                                                                                                                                                           AGCCGAAGCTGGTATCACTGGCACCTGGTATAACCAACTGGGGTCGACTT
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Epenetos,A.A., Spooner,R.A. and Deor COMPOUNDS FOR TARGETING
PATENT: WO 9415644-A 6 21-JUL-1994;
IMP CANCER RES TECH (GB)
Other publication GB 2289679 951129
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Search time (sec): 73.800000
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US-09-589-870-2
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/cgn2_2/gcgdata/geneseq/geneseqn/NA1994.DAT: 072294
                                              alignment_scores:
Quality:
                                                                                                                                                                                                                     The present invention describes a fibrinogen-converting enzyme fusion correction (FCE). The fusion protein is a multidomain protein comprising: (a) a FCE; and (b) a first member of a binding pair, that is linked to the FCE chain: (i) directly by bonds utilizing the N-terminal amino correct constant in the creation of the FCE chain (ii) directly by bonds utilizing the N-terminal amino correct constant interest proups or side-chain functionalities; (c) (ii) via a bifunctional linkage molety linking the groups or correct constant interest produced in the binding pair, where the second member of the binding pair where the second member of the binding pair is covalently attached to the first polypeptide chain. The FCE can be cused in a method for producing fibrin. Fibrin is useful as a sealant in surgery to, e.g. reduce bleeding by sealing blood vessels, and tissues considered the fibrin sealant in the fibrinogen converting converting enzyme from the fibrin sealant preparation via the binding of streptayddin to a biotin solid support. The present sequence encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Avidin;
hybrid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A fibrinogen-converting enzyme fusion protein
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P-PSDB; Y17868.
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                                                                                                                                                      G; 70 T; 0 other;
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1 MetArgLysIleValValAlaAlaIleAlaValSerLeuThrThrValSe

17

from: 1

to:

552

x X80198

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seq_name:
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                                              Kapulnik Y, Ginzberg
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                                                                                                                                                                                                                                               Streptomyces avidinii.
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P-PSDB;
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                                                                                                                                               30-JUL-1999;
                                                                                                                                                                               17-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAGAAGGCCGGCGTCAACAACGGCAACCCCGCTCGACGCCGTTCAGCAG
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        yrAspSerAlaProAlaThrAspGlySerGlyThrAlaLeuGlyTrpThr
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Degeneration of somatic plant tissue by expression of a heterologous protein, useful for controlling plant development and morphology, such as decreasing the number of flowers present to increase the number of fruit -
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Examples; Page 84; 91pp; English

The invention relates to a method of effecting degeneration of a somatic plant tissue by expressing a heterologous protein capable of binding a plant essential factor (PEF), in somatic plant tissue cells, where heterologous protein expression causes depletion of the PEF so the plant viability is maintained, while simultaneous degeneration of the somatic plant tissue is effected. This sequence represents the Streptomyces avidini sps gene as an example of the heterologous gene introduced into the plants. The methods can provide for the selective and optionally reversible cell degeneration in somatic plant tissue. They can be used for artificially controlling plant development and morphology. They can be used e.g. to decrease the number of flowers in fruit producing plants so as to increase the number of fruits which reach maturity.

Sequence 563 BP; 107 A; 213 C; 169 G; 74 T; 0 other;

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alignment_scores:
   Quality:
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Percent Similarity:
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HisaspThrPheThrLysValLysProSeralaAlaSerIleaspAlaAl
                                          alSerAlaAlaGluAlaGlyIleThrGlyThrTrpTyrAsnGlnLeuGly
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                                                                                       rGlyGlnTyrValGlyGlyAlaGluAlaArgIleAsnThrGlnTrpLeuL
                                                                                                                                                                                             rGluSerAlaValGlyAsnAlaGluSerArgTyrValLeuThrGlyArgT
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                                                                                                                                                                                                                                                                                                                      TCTCGGCCGCCGAGGCCGGCATCACCGGCACCTGGTACAACCAGCTCGGC
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Section of the sectio

460

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seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1997.DAT:T73193
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                                     This DNA sequence encodes a streptavidin which is used in a novel method of reducing interference from non-specific binding in assays. Muteins constructed from a core streptavidin or avidin sequence are selected that differ from the native polypeptide by at least one amino acid and have a binding affinity for biotin of less than 1010 1/mole. The biotin-bindable polypeptide may be present as a polymeric conjugate, e.g. with another polypeptide or protein, especially bovine serum albumin. These muteins are used as anti-interference reagents for reducing and/or avoiding nonspecific interactions in a process for detecting an analyte. In particular, they are used in assays where the streptavidin/avidin-biotin specific binding pair is involved for qualitative and/or quantitative determination of an analyte in a test sample, e.g. a heterogeneous affinity for blotin, the muteins have high immunological cross-reactivity with patricular and suriding
                                                                                                                                                                                                                                                           Disclosure; Page 16-17; 26pp; German.
                                                                                                                                                                                                                                                                                                     Streptavidin and avidin muteins with reduced binding affinity for blotin - useful for reducing interference from nonspecific binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-482043/45
                                                                                                                                                                                                                                                                                                                                                                                              Schmitt U;
                                                                                                                                                                                                                                                                                                                                                                                                           Brandstetter H,
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                                                                                                                                                                                                                                                                                          in assays
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alignment\_scores:

Sequence 638

BP;

115 A;

244 C; 193 G; 86

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0 other;

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alignment_block:
US-09-589-870-2 x T73193
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Ratio: 5.115
Percent Similarity: 100.000
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                                                                                                                                                S. avidinii streptavidin cDNA.
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                                                                                                                                                                            (first entry)
                                                                          avidinii.
                                                                                                      ligand; binding affinity; mutant; isolation; recover; immobilise; ss.
   /*tag=
50..121
                                50..601
                                            Location/Qualifiers
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alignment_block:
                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: V34714
                                                                                                                                                                                                                                                                                                                                     US-09-589-870-2 x V34714
                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence encodes a wild-type streptavidin protein isolated from Streptomyces avidinii. This sequence is used to produce mutants which are used in a method to assay the binding affinity of streptavidin mutants. These mutants have a mutation within the amino acid (aa) region 44-53 of the wild-type protein show a higher binding affinity than the wild-type for peptide ligands that include the sequence of formula Trp-X-His-Pro-Gln-Phe-Y-Z where X = any aa; Y and Z are both Gly, or Y = Glu and Z = Arg or Lys. Recombinant streptavidin mutants can be used to isolate, purify and determine proteins or to determine/recover substances that contain streptavidin-binding groups. Such compounds may also be used to immobilise fusions on microtitre plates, microbeads or
                                                             200
                                                                                                                        150
                                                                                                                                                                                    100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptavidin mutants with higher binding affinity for peptide ligands - have mutation in amino acid region 44-53, used to 1. purify or determine fusion proteins including these ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This sequence does not appear in the specification make the mutant streptavidin sequence represented in V347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Skerra A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mat_peptide
                               67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-APR-1998
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                                                                                                                                                                                                                                          rGluSerAlaValGlyAsnAlaGluSerArgTyrValLeuThrGlyArgT
                                                                                                                                                                               GATTACGGCCAGCGCTTCGGCAGACCCCTCCAAGGACTCGAAGGCCCAGG
CGAGTCGGCCGTCGGCAACGCCGAGAGCCGCTACGTCCTGACCGGTCGTT
                                                          TCGACCTTCATCGTGACCGCGGGGGGCGCCGACGGCGCCCTGACCGGAACCTA
                                                                         SerThrPheIleValThrAlaGlyAlaAspGlyAlaLeuThrGlyThrTy
                                                                                                                     TCTCGGCCGAGGCCGGCATCACCGGCACCTGGTACAACCAGCTCGGC
                                                                                                                                        alSerAlaAlaGluAlaGlyIleThrGlyThrTrpTyrAsnGlnLeuGly
                                                                                                                                                                                                 rIleThrAlaSerAlaAserAlaAspProSerLysAspSerLysAlaGlnV 34
                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97EP-0117504
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5.115
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122..598
/*tag= c
/product=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 C;
                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     used to 
V34716.
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seq_documentation_block:
ID Z49867 standard; cDNA; 638 BP
XX

AC Z49867;

XX

DT 25-APR-2000 (first entry)
XX

DT 25-APR-2000 (first entry)
XX

Streptavidin gene for recombi
XX

Potato proteinase inhibitor-I
KW potato proteinase inhibitor-I
KW insect; plant-noxious protein
KW grub; beetle; fly; thrip; loc
XX

Synthetic.

XX

Synthetic.

XX

FH Key cDS

FT cDS

FT sig_peptide for.21

FT sig_peptide for.21

FT sig_peptide for.22.598

FT mat_peptide for.22.598

FT mat_peptide for.331002.

XX

PD 27-JAN-2000.

XX

XX

PD 27-JAN-2000.

XX

XX

PD 27-JAN-2000.

XX

PD 15-JUL-1998; 99WO-NZ00110.

XX

PR 15-JUL-1998; 98NZ-0331002.

XX

PR 15-JUL-1998; 98NZ-031100.

XX

PR 15-JUL-1998; 98NZ-031002.

XX

PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptavidin gene for recombinant pART27 vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          euThrSerGlyThrThrGluAlaAsnAlaTrpLysSerThrLeuValGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rGlyGlnTyrValGlyGlyAlaGluAlaArgIleAsnThrGlnTrpLeuL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGGCCAGTACGTCGGCGGCGCCGAGGCGAGGATCAACACCCAGTGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGGCCTGGAAGAATAACTACCGCAACGCCCACTCCGCGACCACGTGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cgn2_2/gcgdata/geneseq/geneseqn/NA2000.DAT:Z49867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Streptavidin protein"
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                                                                                                                                                                                                                                                                                                                 Murray C,
                                                                                                                                                                                                                                                                                                                    Markwick
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                                                                                                                                                                                                                                                                                                                    Philip
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New chimeric polypeptide and composition useful for conferring pest resistance on

comprising plants -

the polypeptide

111pp; English

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alignment_block:
US-09-589-870-2 x Z49867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             resistance in plants, plant derived products and stored harvest material. Pests that can be controlled include, cotton bollworm, tropical army-worm, European corn-borer or red mitte, tobacco horn worm, loopers, rice stem borer, porina, cutworms, diamondback moth, potato tuber moth, codiling moth, Indian meal moth, gypsy moth, argentine stem weevil, clover root weevil, grass-grubs, corn rootworm, rice and wheat weevils, mealworms, flour beetles, black field cricket, locusts, sawfiles, Western flower thrips, Hessian files or two-spotted mite.
                                                                                                                                             450
                                                                                                                                                                                    134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 express a chimeric polypeptide comprising streptavidin mature peptide fused to the potato proteinase inhibitor-II (PPI-II) signal peptide. The binary vector is targetted to the vacuole by PPI-II signal sequence. Transformation of plant genome with the vector can produce pest
                 167
                                                                                                    151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes streptavidin, a plant-noxious protein. This used in the preparation of a recombinant vector, pART27 designed to
                                                                                                                                                                                                                                                                                                                                                                                                                                    84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality: 936.00
Ratio: 5.115
Similarity: 100.000
                                                                                                                                                                                                                                                                                                          aLysLysAlaGlyValAsnAsnGlyAsnProLeuAspAlaValGlnGln 183
                                                                               H1SASpThrPheThrLySValLySProSerAlaAlaSerIleAspAlaAl 167
                                                                                                                                                                                                                                                                                                                                                                                         rGluSerAlaValGlyAsnAlaGluSerArgTyrValLeuThrGlyArgT
                                                            CACGACACCTTCACCAAGGTGAAGCCGTCCGCCCTCCATCGACGCGGC
                                                                                                                                             TGACCTCCGGCACCACCGAGGCCAACGCCTGGAAGTCCACGCTGGTCGGC
                                                                                                                                                                   euThrSerGlyThrThrGluAlaAsnAlaTrpLysSerThrLeuValGly
                                                                                                                                                                                                                             CGGCCAGTACGTCGGCGCGCGCCGAGGCGAGGATCAACACCCAGTGGCTGC
                                                                                                                                                                                                                                                  rGlyGlnTyrValGlyGlyAlaGluAlaArgIleAsnThrGlnTrpLcuL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCGACCTTCATCGTGACCGCGGGGGGCGCCGACGGCGCCCTGACCGGAACCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerThrPheIleValThrAlaGlyAlaAspGlyAlaLeuThrGlyThrTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTCGGCCGCGAGGCCGGCATCACCGGCACCTGGTACAACCAGCTCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              638
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seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1986.DAT:N60626
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17 rIleThrAlaSerAlaSerAlaAspProSerLysAspSerLysAlaGlnV

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seq_documentation_block:
ID N86626 standard; DNA,
AC N66626;
XX N60626;
XX Squence of a portion
DE Sequence of a portion
DE POLypeptide.
XX Antibiotic; blotin b.
XX Streptomyces.
XX Antibiotic; blotin b.
XX Streptomyces.
XX HARL
FT CDS 481.
FT CDS 480.
FT CD
                                                                                                                                                                alignment_block:
US-09-589-870-2 x N60626
                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                 Quality: 936.00
Ratio: 5.115
Percent Similarity: 100.000
                                                                                                          Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The inventors claim the DNA sequence in SA307 which codes for a steptavidin-like polypeptide (see N602), and the polypeptide encoded by it (P60625). They also claim hybrid SOs comprising N6 and a second sequence coding for another protein, polypeptide, peptide or AA (pref. tissue plasminogen activator (TPA)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA sequences and hybrid DNA sequences - streptavidin-like polypeptide, also joine e.g. tissue plasminogen activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N60626 standard; DNA;
480 ATGCGCAAGATCGTCGTTGCAGCCATCGCCGTTTCCCTGACCACGGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1131 BP; 199 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig. 2;
                       1 MetArgLysIleValValAlaAlaIleAlaValSerLeuThrThrValSe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Garwin JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          biotin binding
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                                                                                                          N60626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84US-0656873
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/note= "p60624"
480..1031
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/note= "P60623"
482..1030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= c
/product= streptavidin-like polypeptide
/note= "P60625"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1131
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                                                                                                                                                                                                                                                                                                                                                                                                                               409 C;
                                                                                                                                                                                                                                                      Gaps: 0
Percent Identity: 100.000
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                                                                                                          to: 1131
                                                                                                                                                                                                                                                                                                                                                                                                                               350 G; 173 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              es - encoding
joined to another
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fusion
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529
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579 50 629

GATTACGGCCAGCGCTTCGGCAGACCCCTCCAAGGACTCGAAGGCCCAGG

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Seq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                              _documentation_block:
z91074 standard; DN
Degeneration of somatic plant tissue by expression of a heterologous protein, useful for controlling plant development and morphology, swass decreasing the number of flowers present to increase the number of
                                                      P-PSDB;
                                                                                                                                                                                                                                                                             Plant somatic tissue degeneration; plant essential factor; depletion; viability; mst gene; plant development; plant morphology; flower; fruit plant; ds.
                                                                                                                                                 03-AUG-1998;
                                                                                                                                                                          30-JUL-1999;
                                                                                                                                                                                                                            WO200007427-A2
                                                                                                                                                                                                                                                      Streptomyces avidinii.
                                                                                                                                                                                                                                                                                                                               Streptomyces avidinii mst gene
                                                                                                                                                                                                                                                                                                                                                            06-JUN-2000
                                                                                                                       (AGRI-) AGRIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 ValAlaTrpLysAsnAsnTyrArgAsnAlaHisSerAlaThrThrTrpSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 yrAspSerAlaProAlaThrAspGlySerGlyThrAlaLeuGlyTrpThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              euThrSerGlyThrThrGluAlaAsnAlaTrpLysSerThrLeuValGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rGlyGlnTyrValGlyGlyAlaGluAlaArgIleAsnThrGlnTrpLeuL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerThrPheIleValThrAlaGlyAlaAspGlyAlaLeuThrGlyThrTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGACCTCCGGCACCACGAGGCCAACGCCTGGAAGTCCACGCTGGTCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGAGTCGGCCGTCGGCAACGCCGAGAGCCGCTACGTCCTGACCGGTCGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCGACCTTCATCGTGACCGCGGGGGCGCCGACGGCCCTGACCGGAACCTA
                                                      2000-195402/17
DB; Y80513.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACGACAGCGCCCCGGCCACCGACGGCACCGCCCTCGGTTGGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_2/gcgdata/geneseq/geneseqn/NA2000.DAT:z91074
                                                                                            Ginzberg
                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                       RES ORG
                                                                                                                                                98IL-0125632
                                                                                                                                                                          99WO-IL00420
                                                                                                                                                                                                                                                                                                                                                                                                              DNA;
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alignment_scores:
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Ratio: 5.115
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: 291074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-589-870-2 x Z91074
                                                                   464
                                                                                                                                     414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a method of effecting degeneration of a somatic plant tissue by expressing a heterologous protein capable of binding a plant essential factor (PEF), in somatic plant tissue cells, where heterologous protein expression causes depletion of the PEF so the plant viability is maintained, while simultaneous degeneration of the somatic plant tissue is effected. This sequence represents the Streptomyces avidinii mst gene as an example of a heterologous gene introduced into the plants. The methods can provide for the selective and optionally reversible cell degeneration in somatic plant tissue. They can be used for artificially controlling plant development and morphology. They can be used e.g. to decrease the number of flowers in fruit producing plants so as to increase the number of fruits which reach maturity.
                                  168
                                                                                                                                                                                                                                                                                                    102
                                                                                                                                                                                                                                                                                                                                       264
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AlaTrpLysAsnAsnTyrArgAsnAlaHisSerAlaThrThrTrpSerGl
                                                                                                                                                                                                                                                                                                                                                                                                                     uSerAlaValGlyAsnAlaGluSerArgTyrValLeuThrGlyArgTyrA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGGCCGCCGAGGCCGCATCACCGGCACCTGGTACAACCAGCTCGGCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         erAlaAlaGluAlaGlyIleThrGlyThrTrpTyrAsnGlnLeuGlySer
                                                                                                                                   CCTCCGGCACCACGAGGCCAACGCCTGGAAGTCCACGCTGGTCGGCCAC
                                                                                                                                                   hrSerGlyThrThrGluAlaAsnAlaTrpLysSerThrLeuValGlyHis 151
                                                                                                                                                                                                   CCAGTACGTCGGCGCGCGAGGCGAGGATCAACACCCAGTGGCTGCTGA
                                                                                                                                                                                                                   yGlnTyrValGlyGlyAlaGluAlaArgIleAsnThrGlnTrpLeuLeuT
                                                                                                                                                                                                                                                                                                                                                       spSerAlaProAlaThrAspGlySerGlyThrAlaLeuGlyTrpThrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCTTCATCGTGACCGCGGGCGCCGACGGCGCCCTGACCGGAACCTACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGCAAGATCGTCGTTGCAGCCATCGCCGTTTCCCTGACCACGGTCTCGAT
                                                                                                                                                                                                                                                                     GCCTGGAAGAATAACTACCGCAACGCCCACTCCGCGACCACGTGGAGCGG
                                                                                                                                                                                                                                                                                                                                     ACAGCGCCCCGGCCACCGACGCCACCGCCCTCGGTTGGACGGTG
                                                                                                                                                                                                                                                                                                                                                                                                     GTCGGCCGTCGGCAACGCCGAGAGCCGCTACGTCCTGACCGGTCGTTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ThrPheIleValThrAlaGlyAlaAspGlyAlaLeuThrGlyThrTyrGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 85; 91pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity:
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100.000
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seq_documentation_block:
ID Q53412 standard; DNA; 552 BP
XX
AC Q53412;
XX
DT 27-JUN-1994 (first entry)
XX
Streptavidin gene.
XX
KW
Streptavidin; protein secret
XX
KW
Streptomyces avidinii.
XX
Key
FT CDS
FT | Location/Qua
FT CDS
FT | Atag- a
FT | mat_peptide | 1..52
FT | sig_peptide | 73..519
FT | sig_peptide | 1..92
FT | misc_feature | 109..519
FT | xtag- a
FT | misc_feature | 109..519
FT | xtag- a
FT | misc_feature | 109..519
FT | xtag- a
FT | misc_feature | 109..519
FT | xtag- a
F
                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
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                                                                                                                                                                                                                                                                            US-09-589-870-2 x Q53412
                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                        Align seg 1/1 to: Q53412 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tetrameric biologically active streptavidin is produced by from Bacillus subtilis transformed with a plasmid encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptavidin prodn. from Bacillus subtilis - using signal protein from bacterial exo-protein and expression element from Gram positive bacterial protein.
     51
                                                      17
MetargLysIleValValAlaAlaIleAlaValSerLeuThrThrValSe
                                                                                                                                                                                                                                                                                                                                                                                       Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein secretion; Bacillus subtilis; ss
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5.093
99.454
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/note= "fused
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                                                                                                                                                                                                                                                                                                                                                             Length: 183
Gaps: 0
Percent Identity: 99.454
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seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1998.DAT:V34715
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                                                                                                                                                                                                  S. avidinii streptavidin mutant #1 DNA.
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                                                                                                                                                                                                                                                                                                             aLysLysAlaGlyValAsnAsnGlyAsnProLeuAspAlaValGlnGln 183
                                                                                                                                                                                                                                                                                                                                         yrAspSerAlaProAlaThrAspGlySerGlyThrAlaLeuGlyTrpThr 100
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                                                                                                                                                                                                                                                                                 GAAGAAGGCCGGCGTCAACAACGGCAACCCGCTCGACGCCGTTCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rGluSerAlaValGlyAsnAlaGluSerArgTyrValLeuThrGlyArgT
                                                                                                                                                                                                                                                                                                                                                                                                                                 ACGACAGCGCCCCGGCCACCGACGGCAGCGGCACCGCCCTCGGTTGGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGAGTCGGCCGTCGGCAACGCCGAGAGCCGCTACGTCCTGACCGGTCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCGACCTTCATCGTGACCGCGGGGGGGCGCGGGGCGCCTGACCGGAACCTA
                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                             ligand; binding affinity; recover; immobilise; ss.
                97EP-0117504
                                                                                                    /*tag= a
50..121
/*tag= b
122..598
                                                                              /*tag= c
/product= Streptavidin
251..262
                                                                                                                                  Location/Qualifiers 50..601
                                                          638
                                                                                                                                                                                                                                              ВP
                                                                                                                                                                                    mutant;
                                                                                                                                                                                    isolation;
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96DE-1041876

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: V34715
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                                                                                                                                                                                                                                                          rGluSerAlaValGlyAsnAlaGluSerArgTyrValLeuThrGlyArgT
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rGlyGlnTyrValGlyGlyAlaGluAlaArgIleAsnThrGlnTrpLeuL 134
                                                                                                                                         ACGACAGCGCCCCGGCCACCGACGGCAGCGGCACCGCCCTCGGTTGGACG
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seq_name:
                                                                                     Streptavidin mutants with higher binding affinity for peptide ligands - have mutation in amino acid region 44-53, used to is purify or determine fusion proteins including these ligands
                                                                                                                                                                                                                                                                                                                                                                                                                     S. avidinii streptavidin mutant #2 DNA.
                                                                                                                                                                                                                                                                                                                                                                            Streptomyces avidinii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        V34716 standard; DNA;
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122..598
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251..262
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ATCGGTGCGAGG"
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This sequence encodes a mutant streptavidin protein isolated from Streptomyces avidinii where the residues ESAV at position 44-47 of the mature wild type sequence are replaced by IGAR. This sequence is used to produce mutants which are used in a method to assay the binding affinity of streptavidin mutants. These mutants have a mutation within the amino acid (aa) region 44-53 of the wild-type protein show a higher binding affinity than the wild-type for peptide ligands that include

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seq_documentation_block:
ID Q70659 standard; DN
XX
AC Q70659;
                                                                              seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1994.DAT:Q70659
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US-09-589-870-2 x V34716
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                                                                                                                                                                               CACGACACCTTCACCAAGGTGAAGCCGTCCGCCGCCTCCATCGACGCGGC
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                                                                                                                                                                                   AlaValGlyAsnAlaGluSerArgTyrValLeuThrGlyArgTyrAspSe
                                                                                                                                     heIleValThrAlaGlyAlaAspGlyAlaLeuThrGlyThrTyrGluSer
rpLysAsnAsnTyrArgAsnAlaHisSerAlaThrThrTrpSerGlyGln 119
                                           ralaProAlaThrAspGlySerGlyThrAlaLeuGlyTrpThrValAlaT 103
                                                                              GCGGTTGGTAACGCAGAATCCCGCTACGTACTGACTGGCCGTTATGACTC
                                                                                                                                                                       AGCCGAAGCTGGTATCACTGGCACCTGGTATAACCAACTGGGGTCGACTT
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seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA2000.DAT:z91076
                     The invention relates to a method of effecting degeneration of a somatic plant tissue by expressing a heterologous protein capable of binding a plant essential factor (PEF), in somatic plant tissue cells, where heterologous protein expression causes depletion of the PEF so the plant viability is maintained, while simultaneous degeneration of the somatic plant tissue is effected. This sequence represents the Streptomyces avidinii mprost gene as an example of a heterologous gene introduced into the plants. The methods can provide for the selective and optionally reversible cell degeneration in somatic plant tissue. They can be used for artificially controlling plant development and morphology. They can be used e.g. to decrease the number of flowers in fruit producing plants
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Z91076 standard; DNA; 495 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Degeneration of somatic plant tissue by expression of a heterologous protein, useful for controlling plant development and morphology, such as decreasing the number of flowers present to increase the number of
                                                                                                                                                                                                                                                                                                                                                                                    Examples; Page 86-87; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant somatic tissue degeneration; viability; mprost gene; plant devel
                                                                                                                                                                                                                                                                                                                                                                                                                                                   fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kapulnik Y, Ginzberg I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces avidinii mprost gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fruit plant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hrPheThrLysValLysProSerAlaAlaSerIleAspAlaAlaLysLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTTTACCAAAGTTAAGCCTTCTGCTGCTAGCATTGATGCTGCCAAGAAA 1302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGCACTACCGAAGCGAATGCATGGAAATCGACACTAGTAGGTCATGACA
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of fruits which reach maturity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         development; plant morphology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plant essential factor; depletion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169
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Sequence 495 BP;

98 A; 188 C; 151 G; 58 T; 0 other;

99WO-IL00420

increase the number

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seq_documentation_block:
ID z91075 standard; DNA;
XX
AC z91075;
XX
DT 06-JUN-2000 (first e
XX
DE Streptomyces avidinii
XX
Plant somatic tissue
KW viability; prost gene
KW viability; ds.
XX
OS Streptomyces avidinii
XX
PN W0200007427-A2.
XX
PD 17-FEB-2000.
XX
30-JUL-1999; 99WO-1
                                                                                                                                                                                                                                                                                                                   seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA2000.DAT:291075
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US-09-589-870-2 x Z91076
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Quality:
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                                                                                                                             Plant somatic tissue degeneration; plant essential factor; depletion; viability; prost gene; plant development; plant morphology; flower; fruit plant; ds.
                                                                                                                                                                                                                                                                                                                                                461
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                                                                                                                                                                                                                                                                                                                                                                                                       411
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                                                                                                    Streptomyces avidinii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 CATCACCGGCACCTGGTACAACCAGCTCGGCTCGACCTTCATCGTGACCG
                                                                                                                                                                                                                                                                                                                                                                                                                    alLysProSerAlaAlaSerIleAspAlaAlaLysLysAlaGlyValAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    yIleThrGlyThrTrpTyrAsnGlnLeuGlySerThrPheIleValThrA 57
                                                                                                                                                                                                                                                                                                                                               AACGGCAACCCGCTCGACGCCGTTCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                    GGCCAACGCCTGGAAGTCCACGCTGGTCGGCCACGACACCTTCACCAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rAspGlySerGlyThrAlaLeuGlyTrpThrValAlaTrpLysAsnAsnT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCGCAACGCCCACTCCGCGACCACGTGGAGCGGCCAGTACGTCGGCGGC
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Gaps:
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alignment_block:
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                                139
                                                                    305
                                                                                                                                                                        106
                                                                                                                                                                                                           205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Degeneration of somatic plant tissue by expression of a heterologous protein, useful for controlling plant development and morphology, such as decreasing the number of flowers present to increase the number of
   355
                                                                                                    123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Examples; Page 86; 91pp; English
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P-PSDB; Y80514.
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GlyAlaGluAlaArgIleAsnThrGlnTrpLeuLeuThrSerGlyThrTh 139
                                                                                                                                                        snTyrArgAsnAlaHisSerAlaThrThrTrpSerGlyGlnTyrValGly 122
                                                                                                                                                                                                                           aThrAspGlySerGlyThrAlaLeuGlyTrpThrValAlaTrpLysAsnA 106
                                                                                                                                                                                                                                                                                                                                                              hrAlaGlyAlaAspGlyAlaLeuThrGlyThrTyrGluSerAlaValGly
                                                                                                                                                                                                                                                                                                                                                                                                                CGGCATCACCGGCACCTGGTACAACCAGCTCGGCTCGACCTTCATCGTGA
                                                                    GGCGCCGAGGCGAGGATCAACACCCAGTGGCTGCTGACCTCCGGCACCAC
                                                                                                                                      ACTACCGCAACGCCCACTCCGCGACCACGTGGAGCGGCCAGTACGTCGGC
                                                                                                                                                                                                         CACCGACGGCAGCGGCACCGCCCTCGGTTGGACGGTGGCCTGGAAGAATA
                                                                                                                                                                                                                                                                           AACGCCGAGAGCCGCTACGTCCTGACCGGTCGTTACGACAGCGCCCCGGC
                                                                                                                                                                                                                                                                                             AsnAlaGluSerArgTyrValLeuThrGlyArgTyrAspSerAlaProAl
                                                                                                                                                                                                                                                                                                                                                CCGCGGGCGCCGACGGCCCCTGACCGGAACCTACGAGTCGGCCGTCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  aGlyIleThrGlyThrTrpTyrAsnGlnLeuGlySerThrPheIleValT 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    492 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 A;
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5.186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 98.758
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seq_documentation_block:
ID N80186 standard; DNA; 498 BF
XX

AC N80186;
XX

Dff 13-OCT-1990 (first entry)
XX

Biosynthetic Antibody Bindir
KW Biosynthetic:
XX

Biosynthetic:
XX

Biosynthetic:
XX

OS Synthetic:
XX

Anti-CEA monoclonal antibody
XX

OS Synthetic:
XX

ON HOB809344-A.
XX

PN WO8809344-A.
XX

O1-DEC-1988:
BRWO-US01737.
XX

PP 19-MAY-1987; 87US-0052800.
XX

CCREA-) CREATIVE BIOMOLECULE
XX

PH 1988-353928/49.
PA (CREA-) CREATIVE BIOMOLECULE
XX

PP 1988-353928/49.
P-PSDB; P80160.
XX

Recombinant multifunctional pr having an antibody binding s
PT ion sequestering or binding
XX

PT having an antibody binding s
PT ion sequestering or binding
XX

Disclosure; ; 115pp; English
XX

Disclosure; pilisp; English
XX

Disclosure; pilisp; English
XX

CC chain BABS and streptavidin
CC See also N80171-N80192.
XX

SQ Sequence 498 BP; 117 A; 137
                                                                                                                                                                                               alignment_block:
US-09-589-870-2 x N80186
                                                                                                                                                                                                                                                                                           alignment_scores:
    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1988.DAT:N80186
                                                                                                                                                           Align seg 1/1
                                                                                                                                                                                                                                                       Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Encodes multi-functional biosynthetic protein comprising single chain BABS and streptavidin protein trailer linked via a spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biosynthetic Antibody Binding site (BABS); variable domain; anti-CEA monoclonal antibody; streptavidin; ss.
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                                                                                                                                                                                                                                                                                                                                                                         Sequence 498 BP; 117 A; 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; ; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant multifunctional protein - having an antibody binding site and a sequence for biological activity, ion sequestering or binding to a solid support.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Encodes biosynthetic protein with streptavidin trailer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CREA-) CREATIVE BIOMOLECULES
                                                                         AsnAsnGlyAsnProLeuAspAlaValGlnGln 183
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Percent Identity:
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S

alThrAlaGlyAlaAspGlyAlaLeuThrGlyThrTyrGluSerAlaVal 71

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seq_name:
                                                                    Preparation of S-layer proteins by expressing sbs-A gene negative bacterium - or new sbs-B gene in any host, also recombinant proteins containing heterologous inserts, e.g epitope(s), useful as vaccines and adjuvants
                                                                                                                                                                                                                                                                                               S-layer; sbs-A; vaccine; adjuvant; carrier; hybridisation molecular spinning nozzle; molecular laser; streptavidin;
                                                                                                                                                                                                                                                                                                                                                                                                                                             454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304
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                                                                                           new
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S-layer structures comprising the novel Bacillus stearothermophilus PV72 S-layer protein, sbs-A, can be used as vaccines or adjuvants, particularly when they include a bacterial ghost that may contain additional epitopes in its membrane. Other uses of recombinant

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US-09-589-870-2 x T75491
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                                                                             158
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                                                                                                                            aAsnAlaTrpLysSerThrLeuValGlyHisAspThrPheThrLysValL
GlyAsnProLeuAspAlaValGlnGln
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                                                                  ysProSerAlaAlaSerIleAspAlaAlaLysLysAlaGlyValAsnAsn
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Minimum DB :
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Copyright (c) 1993 - 2000 Compugen Ltd.
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avidin-related pro
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flagellin - Escher
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190K surface antig
membrane glycoprot
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probable hydrolase
cellulase (EC 3.2.
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streptavidin v1 pr
streptavidin v2 pr
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high-molecular-wei
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of avidin and streptavidin. Tyrosine

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A;Status; preliminary
A;Molecule type: DNA
A;Residues: 1-183 <ARG>
A;Cross-references: GB:X03591; NID:946740; PIDN:CAA27265.1; PID:946741
A;Cross-references: GB:X03591; NID:946740; PIDN:CAA27265.1; PID:946741
A;Cross-references: GB:X03591; NID:946740; MID:946740; MID:94
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Best Local Similarity
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181
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                                          1 VQQ 183
VQQ
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Pred. No. 8.7e-67;
); Mismatches 0;
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RESULT

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streptavidin v2 precursor - Streptomyces venezuelae
C;Species: Streptomyces venezuelae
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_chan
C;Accession: S57285
R;Bayer, E.A.; Kulik, T.; Adar, R.; Wilchek, M.
Biochim. Biophys. Acta 1263, 60-66, 1995
A;Title: Close similarity among streptavidin-like, biotin-bir
A;Reference number: S57284; MUID:95359204
A;Accession: S57285
A;Molecule type: DNA
A;Residues: 1-183 CBAY>
A;Experiamily: streptavidin
C;Superfamily: streptavidin
C;Superfamily: streptavidin
F;1-24/Domain: signal sequence #status predicted <MAT>
F;25-183/Product: streptavidin v2 #status predicted <MAT>
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C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_chan
C;Accession: S57284
R;Bayer, E.A.; Kullk, T.; Adar, R.; Wilchek, M.
Biochim. Biophys. Acta 1263, 60-66, 1995
A;Title: Close similarity among streptavidin-like, biotin-bin
A;Reference number: S57284; MUID:95359204
A;Accession: S57284
A;Accession: S57284
A;Molecule type: DNA
A;Residues: 1-183 <BAY>
A;Experimental source: Strain Tue2460
C;Superfamily: streptavidin
F;1-24/Domain: signal sequence #status predicted <MaT>
F;25-183/Product: streptavidin v1 #status predicted <MAT>
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                                                                                                                                                                   VGGAEARINTQWLLTSGTTEANAWKSTLVGHDTFTKVKPSAASIDAAKKAGVNNGNPLDA 180
                                                                                                               GALTGTYESAVGNAESRYVLTGRYDSAPATDGSGTALGWTVAWKNNYRNAHSATTWSGQY
              VAGSEARINTQWILTSGTTAANAWKSTLVGHDTFTKVKPSAASIDAAKKAGVNNGNPLDA
                                                                                        GSLTGTYESAVGNAESRYVLTGRYDSAPATDGSGTALGWTVAWKNNYRNAHSATTWSGQY 120
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Pred. No. 1e-63;
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A; Genetics: CH1
A; Accession: S42205
A; Molecule type: DNA
A; Residues: 1-150 <KEW>
A; Cross-references: EMBL: Z22882; NID: g311812
A; Experimental source: strain White Leghorn; ti
A; Genetics: CH2
C; Genetics: CH1>
A;Molecule type: DNA
A;Residues: 1-21, S',23-152 <WAL>
A;Residues: 1-21, S',23-152 <WAL>
A;Cross-references: GB:L27818; NID:g450255; PID:g451889
A;Experimental source: adult oviduct, strain White Leghorn
A;Note: difference at position 22 may be due to PCR error
                                                                                                                                        avidin precursor [validated] - chicken C;Species: Gallus gallus (chicken) C;Species: Gallus gallus (chicken) C;Date: 24-Apr-1984 #sequence_revision 04-Nov-1994 #text_change 15-Sep-2000 C;Accession: A54975; A27518; A92093; A92092; A03160 R;Wallen, M.J.; Laukkanen, M.O.; Kulomaa, M.S. submitted to GenBank, January 1994 A;Description: Sequence of the chicken egg-white avidin gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Introns: 27/3; 96/1; 136/2

C;Superfamily: avidin

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-150/Product: avidin related protein 4/5 #status pr

F;28-105/Disulfide bonds: #status predicted
                                                                                                         A; Reference number: A54975
A; Accession: A54975
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C;Genetics: <CH2>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATDGSGTALGWTYAWKNNYRNAHSATTWSGQYY---GGAEARINTQWLLTSGTTEAN-AW 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSARKCSLTGKWTNNLGSIMTIRAVNSRGEFTGTYLTAVADNPGNITLSPLLGIQHKRA- 81
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33.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
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Pred. No. 7.5e-05;
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        in
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19;

Gaps

8

gene sequence

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avidin-related protein 4/5 precursor - chicken c/Species: Gallus gallus (chicken) c/Species: Gallus gallus (chicken) c/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 07-May-1999 c/Accession: S42204; S42205 R.Keinaenen, R.A.; Wallen, M.J.; Kristo, P.A.; Laukkanen, M.O.; Toimela, T./Bur. J. Biochem. 220, 615-621, 1994 A.Title: Molecular cloning and nucleotide sequence of chicken avidin-related A;Reference number: S42201; MUID:94170814 A;Accession: S42204 A;Molecule type: DNA A;Residues: 1-150 <KEI> A;Cross-references: EMBL: Z22883; NID:9311811 A;Cross-references: EMBL: Z22883; NID:9311811
                                                                                                                                                                                                                              sequence of chicken avidin-related genes 1-
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A;Introns: 27/3; 98/1; 138/2
C;Superfamily: avidin
C;Keywords: glycoprotein
C;Keywords: signal sequence #status predicted <SIG>
F;1-24/Domain: signal sequence #status experimental <MAT>
F;25-152/Product: avidin #status experimental <MAT>
F;28-107/Disulfide bonds: #status experimental
F;41/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: A51448; PDB:2AVI
A;Contents: annotation; X-ray crystallography, 3.0 angstroms, with biotin, res
R;Livnah, O; Bayer, E.A.; Wilchek, M.; Sussman, J.L.
Proc. Natl. Acad. Sci. U.S.A. 90, 5076-5080, 1993
A;Title: Three-dimensional structures of avidin and the avidin-biotin complex.
A;Reference number: A47554; MUID:93281699
A;Contents: annotation; X-ray crystallography, 3.0 angstroms
R;Pugliese, L.; Coda, A.; Malcovati, M.; Bolognesi, M.
submitted to the Brookhaven Protein Data Bank, March 1993
A;Reference number: A5162; PDB:1AVD
A;Contents: annotation; X-ray crystallography, 2.7 angstroms, with biotin, res
R;Pugliese, L.; Coda, A.; Malcovati, M.; Bolognesi, M.
submitted to the Brookhaven Protein Data Bank, March 1993
A;Reference number: A51623; PDB:1AVE
A;Reference number: A51623; PDB:1AVE
A;Reference number: A51623; PDB:1AVE
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A; Residues: 25-57, Tr, 59-76, Er, 78-152 <DEL>
A; Experimental source: egg white
A:Note: approximately 50% of the chains have 58-Ile
R:Huang, T.S.; DeLange, R.J.
J. Blol. Chem. 246, 686-697, 1971
A;Title: Egg white avidin. II. Isolation, composition.
A; Reference number: A92092, MUID:71107557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Gope, M.L.; Keinaenen, R.A.; Kristo, P.A.; Conneely, O.M.; Nucleic Acids Res. 15, 3595-3606, 1987
A;Title: Molecular cloning of the chicken avidin cDNA.
A;Reference number: A27518; MUID:87203384
A;Accession: A27518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 25-57, 'T',59-76,'E',78-152 <DEL2>
R;Livnah, O.; Susman, J.
submitted to the Brookhayen Protein Data Bank, April 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;DeLange, R.J.; Huang, T.S.
J. Biol. Chem. 246, 698-709, 1971
A;Title: Egg white avidin. III. Sequence of the 78-residue middle cyanogen bromide A;Reference number: A92093; MUID:71107558
A;Accession: A92093
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R:Pugliese, L.; Coda, A.; Malcovati, M.; J. Mol. Biol. 231, 698-710, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Contents: sequences of tryptic peptides A; Accession: A92092
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A; Residues: 1-152 <GOP>
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contents: annotation;
                             137
                                                                                147 TLVGHDTFTKVK 158
                                                                                                                                                                                      93
                                                                                                                                                                                                                                                                    34 VSAAEAGITGTWYNQLGSTFIVTA-GADGALTGTYESAVGNAESRYVLIGRYDSAPATDG
                                                                                                                                   82
                                                                                                                                                                                                                                       23
                             TRVGINIFTRLR 148
                                                                                                                                                                                                                                       LSARKCSLTGKWTNDLGSNMTIGAVNSRGEFTGTYITAV-TATSNEIKESPLHGTQNTIN 81
                                                                                                                                   KRTQPTFGFTVNWK----
                                                                                                                                                                                 SGT--ALGWTVAWKNNYRNAHSATTWSGQYV---GGAEARINTQWLLTSGTTE-ANAWKS 146
                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  x-ray crystallography,
                                                                                                                                                                                                                                                                                                                                                                   15.3%;
                                                                                                                                   FSESTTVFTGQCFIDRNGKEV-LKTMWLLRSSVNDIGDDWKA
                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                   Score 143.5; DB Pred. No. 0.0001
                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           composition, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIDN:CAA28954.1; PID:g63072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.7
                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                             56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  angstroms
                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                             Length 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beattle, W.G.; Zarucki-Sch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    without biotin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         with biotin, residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       with biotin, residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      form of egg-white avidin
                                                                                                                                                                                                                                                                                                                                          13;
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                             92
                                                                                                                                                                                                                                                                                                                                          7;
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S42203
A; Gene: avr3
A; Introns: 27/3; 96/1; 136/2
C; Superfamily: avidin
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A;Cross-references: EMBL:Z21611
C;GenetLcs:
A;Introns: 27/3; 96/1; 136/2
C;Superfamily: avidin
C;Keywords: glycoprotein
C;Keywords: glycoprotein
F;1-24/Domain: signal sequence #status predicted <SIG>F;2-150/Product: avidin-related protein 1 #status predicted <MAT>F;28-105/Disulfide bonds: #status predicted
F;54,67,93/Binding site: carbohydrate (Asn) (covalent) #status predicted
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R;Keinaenen, R.A.; Wallen, M.J.; Kristo, P.A.; Laukkanen, M.O.; Toimela, T.A.;
Eur. J. Biochem. 220, 615-621, 1994

A;Title: Molecular cloning and nucleotide sequence of chicken avidin-related ge
A;Reference number: $42201; MUID:94170814

A;Accession: $42201

A;Status: preliminary
                                                                                                                A;Cross-references: EMBL:Z21612; NID:g65432
R;Kunnas, T.A.; Wallen, M.J.; Kulomaa, M.S.
Biochim. Biophys. Acta 1216, 441-445, 1993
A;Title: Induction of chicken avidin and related A;Reference number: S39799; MUID:94092737
A;Accession: S39800
                                                                                                                                                                                                                                                                                               C;Accession: $42203; $39800
R;Keinaenen, R.A.; Wallen, M.J.; Kristo, P.A.; Laukkanen, M.O.; Toimela, T.A.; Heleni Eur. J. Biochem. 220, 615-621, 1994
A;Title: Molecular cloning and nucleotide sequence of chicken avidin-related genes 1-A;Reference number: $42201; MUID:94170814
A;Accession: $42203
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-150 <KEID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               avidin-related protein 3 precursor - chicken
N;Alternate names: avr3 proteiin
C;Species: Gallus gallus (chicken)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Gallus gallus (chicken)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 07-May-1999
                        A;Status: preliminary; translation
A;Molecule type: mRNA
A;Residues: 71-150 <KUN>
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A; Residues: 1-150 <KEI>
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A; Cross-references: EMBL: Z21536;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 DWKATRVGNNDFTR 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 VSAAEAGITGTWYNOLGSTFIVTAGA---DGALTGTYESAV----GNAESRYVLTGRYDS 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AWKSTLVGHDTFTK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A-----CQPTFGFTVHW--NF--SESTSVFVGQCFVDKSGKEV-LKTKWLQRLAVDDISD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APATDGSGTALGWTVAWKNNYRNAHSATTWSGQ-YV--GGAEARINTQWLLTSGTTE-AN 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.0%; Score 121.5; DB 2; 32.8%; Pred. No. 0.0069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24; Mismatches
NID: g65429
                                                                                          not shown
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                                                                                                                                                                                  mRNAS
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                                                                                                                                                                                     infection
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A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-114 <DEL>
A; Cross-references: GB:X17530; NID:g10225; PID:g667061
A; Accession: B40136
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: DNA
A; Residues: 181-251, 329-370, 'R', 372-408, 'RA', 411-441 <DE2>
A; Accession: C40136
A; Residues: C40136
A; Status: preliminary; not compared with conceptual translation
A; Status: preliminary; not compared with conceptual translation
A; Status: preliminary; not compared with conceptual translation
A; Residues: 'K', 747-821, 898-978 <DE3>
R; Hursh, D. A.; Andrews, M.E.; Raff, R.A.
Science 237, 1487-1490, 1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: A sea urchin gene encodes a polypeption A; Reference number: A29316; MUID:87319677
A; Accession: A29316
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 'S', 280-481, 786-1064 <HUR>
A; Cross references: GB:M17421; NID:g161474; PI: R; Hunt, L.T.; Barker, W.C.
R; Hunt, L.T.; Barker, W.C.
                                                                                                                                                                                                                                             C;Superfamily: Clr/Cls repeat homology; EGF homology F;1-19/Domain: signal sequence #status predicted <SIG> F;20-1064/Product: fibropellin: #status predicted <FII
                                                                  F; 256-287/Domain: F; 294-325/Domain:
                                                                                                                                    F;218-249/Domain:
                                                                                                                                                                F;180-211/Domain:
                                                                                                                                                                                            F;57-175/Domain: Clr/Cls repeat homology
                                                                                                                                                                                                                               F;23-54/Domain: EGF homology <EG01>
                                                                                                                                                                                                                                                                                                                                                                FASEB J. 3, 1760-1764, 1989
A;Title: Avidin-like domain
A;Reference number: A43131;
A;Contents: annotation
C;Comment: EGF homology repe
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N;Alternate names: epidermal growth factor homolog precursor
N;Contains: alternatively spliced fibropellin Ib (EGFI)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 13-May-1992 #sequence_revision 17-Sep-1997 #text_change 21-Jul-2000
C;Accession: A40136; B40136; C40136; A29316; A43313
R;Delgadillo-Reynoso, M:G:; Rollo, D.R.; Hursh, D.A.; Raff, R.A.
J. Mol. Evol. 29, 314-327, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Structural analysis of the uEGF gene A;Reference number: A40136; MUID:90112459 A;Accession: A40136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----CQPTFGFTVHW--NF--SESTSVFVGQCFIDRSGKEV-LKTKWLQRLAVDDISDDW 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATDGSGTALGWTYAWKNNYRNAHSATTWSGQYY----GGAEARINTQWLLISGTTE-ANAW 144
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EGF
EGF
EGF
                                                                                                                                                                   EGF
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                        F homology <EG02>
F homology <EG03>
F homology <EG04>
F homology <EG05>
F homology <EG06>
homology
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MUID:89196806
<EG07>
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Pred. No. 0.0
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N;Alternate names: avr2 protein
C;Species: Gallus gallus (chicken)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 07-May-1999
C;Accession: S42202; S39799
C;Accession: S42202; S39799
R;Keinaenen, R.A.; Wallen, M.J.; Kristo, P.A.; Laukkanen, M.O.; Toimela, T.A.; Helen Bur. J. Blochem. 220, 615-621, 1994
A;Title: Molecular cloning and nucleotide sequence of chicken avidin-related genes
A:Paference number: S42201; MUID:94170814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;448-439/Domain: 1
F;446-477/Domain: 1
F;484-515/Domain: 1
F;522-553/Domain: 1
A:Introns: 27/3; 96/1; 136/2
C;Superfamily: avidin
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-150/Product: avidin-related protein 2 #status predicted
F;28-105/Disulfide bonds: #status predicted
                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 71-150 < KUN>
                                                                                                                                                                                                                                                    A; Reference number: A; Accession: S39799
                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:Z21554; NID:g65430
R;Kunnas, T.A.; Wallen, M.J.; Kulomaa, M.S.
Biochim. Biophys. Acta 1216, 441-445, 1993
A;Title: Induction of chicken avidin and related mRNAs after bacterial infection.
A;Reference number: S39799; MUID:94092737
                                                                                                                                            C; Genetics:
                                                                                                                                                                A; Cross-references:
                                                                                                                                                                                                                           A; Status: preliminary; translation
                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-150 <KEI>
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                                                                                                                     A;Gene: avr2
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57,451-466,468-477,484-495/Disulfide bonds: #status predicted
F;489-504,506-515,522-533,527-542,544-553,560-571,565-580,582-591,598-609,603-618,620
08,810-819,826-837,831-846,848-857,864-875,869-884,886-895,902-913,907-922,924-933/Di
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F;936-1064/Region:
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F;636-667/Domain:
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Best Local S
Matches 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1039 DIKKSNMVGQDKWTRYEQSIA 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 NAWKSTLVGHDTFTKVKPSAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YDF-----PSFGFTVV----RDNGQSTTSWTGQCHLCDGEEVLYTTWINTNMVSTCQ 1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VNCEEVGFCDLEGMWYNECNDQVTITKTSTGMMLGDYMTYNERALGYAAPTVVVGYASNN 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSAAEAG---ITGTWYNQLGSTFIVTAGADGALTGTY----ESAVGNAESRYVL---TGR 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40;
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                                                                                                                                                            EMBL: Z21535; NID: g65428
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Pred. No. 0.
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flagellin - Escherichia coli (strain Su 1242)

(;Species: Escherichia coli

C;Species: Escherichia coli

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 26-Aug-1999

C;Accession: B48658

R;Schoenhals, G.; Whitfield, C.

J. Bacteriol. 175, 5395-5402, 1993

A;Title: Comparative analysis of flagellin sequences from Escherichia coli :
A;Reference number: A48658; MUID:93374833

A;Accession: B48658
A;Scatus: preliminary
A;Molecule type: DNA
A;Residues: 1-595 <SCH>
A;Cross-references: GB:107387; NID:9290436; PIDN:AAA23797.1; PID:9290437
A;Cross-references: GB:107387; NID:9290436; PIDN:AAA23797.1; PID:9290437
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J. Bacteriol. 175, 5395-5402, 1993
A;Title: Comparative analysis of flagellin sequences
A;Reference number: A48658; MUID:93374833
A;Accession: A48658
A;Status: preliminary
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C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change
C;Accession: A48658
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C; Superfamily: flagellin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          flagellin - Escherichia coli (strain Bi 316-42)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 32.8 Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                            522
                                                                                                                                                                                                                                                                                                                                                                                                                   158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y Match 12.0%; Score 112; DB Local Similarity 26.1%; Pred. No. 0.16; hes 52; Conservative 30; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                            RPSLGAIQNRLDSAVTNLN 540
                                                                                                                                                                                                                                                                                                                                                                                                                 KPSAASIDAAKKAGVNNGN 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNGKVTVDSGTGTGKYAPKVGAEVYVSANGTLTTDATSEGTVTKDPLKALDEAISSIDKF 521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTYESAV-----GNAESRYVLTGRYDSAPAT----DGSGTALG-WTVAWK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASVTMGGTTYNFKTGADAD-AATANAGVSFTDTASKETVLNKVATAKQGKAVAADGDTSA 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APATDGSGTALGWTVAWKNNYRNAHSATTWSGQ-YV--GGAEARINTQWLLTSGTTE-AN 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSARKCSLTGEWDNDLGS--IMTIGAVNDNGEFDGTYITAVADNPGNITLSPLLGIQHKR 80
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paracrystalline surface layer protein RsaA - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: A48995
Can. J. Microbiol. 38, 193-202, 1992
A;Title: Nuclectide sequence analysis of the gene encoding the Caulobacter crescentum A;Reference number: A48995; MUID:93007489
A;Reference number: A48995; MUID:93007489
A;Rocession: A48995
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-1026 GGIL>
A;Residues: 1-1026 GGIL>
A;Residues: 1-1026 GGIL>
A;Rosyerimental source: CBISA, ATCC 19089
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:116173, NCBIP:116174)
RESULT 13
B43855
high-molecular-weight surface-exposed protein - Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C;Accession: B43855
C;Accession: B43855
R;Barenkamp, S.J.; Leininger, E.
R;Barenkamp, S.J.; Leininger, E.
R;Barenkamp, S.J.; Leininger, E.
A;Title: Cloning, expression, and DNA sequence analysis of genes encoding nodetalla pertussis.
detalla pertussis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 AAIAVSLTTVSITASASADPSKDSKAQVSAAEAGITGTWYNQLGST---FIVTAGADGAL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 VAAIAVSLTTVSITASASADPSKDSKAQV----SAAEAGITGTWYNQLGSTFIVTAGADG 61
                                                                                                                                                                                                                                                                                                                                                                      TTTGAIAVTGGTA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VQAAAVTALPTGVTISGIETMNVTSGAAITLNTSSGVTGLTALNTNTSGAAQTVTAGAGQ 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KPSAASIDAAKKAGVNNGN 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITYKSGVQTYQAVFAAGDGTASAKYADNTDVSNATATYTDADGEMTTIGSYTTKYSIDA 461
                                                                                                                                                                                                                                                                                    AGATVAGRVNG
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                                                                                                                                                                                                                                                                                                                                                                                                               TWSGQY-VGGAEARINTQWLLTSGTTEANAWKSTLVGHD-----TFTKVKPSAASI 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTGTYESAV-----GNAESRYVLTGRYDSAPATDGSGTALGWTVAWKNNYRNAHSAT 114
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                                           and DNA sequence analysis of genes encoding nontypeable
                                                                                                                                                                                                                                                                                                                                                                        VTVAQTAGNAVNTTLTQADVTVTGNSSTTAVTVTQTAAAT 466
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-2468 <STO>
A;Cross-references: GB:AE004613; GB:AE004091; NID:g9947856; PIDN:AAG05263.1; GSPDB:GN001
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C:Accession: A83412
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor, Reference number: A82950 A; Accession: A83412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein PA1874 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 15-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: PA1874
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1477 <BAR>
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Best Local S
Matches 61
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Best Local Similarity
Matches 50; Conserv
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                                                                    1543 NGTVINAVAQDPAGNTSGPASVTVDAIAPPAPVINPSNGVVISGTAEAGATVILTDGNGN 160:
                                                                                                                                                                                                                                    1439 PIGQVTADGSGNWSFTPGIPLPDGTVVNVVARSPS-----NVDSAPAVITVDGVAPAAP 1492
                                                                                                                                                              1493 VIDPSNGTEISGTAEAGATVI-
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                                      177 PLDAV 181
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                                                                                                                                                                                                                                                                                         59
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                     NAWKSTLYGHDTFTKVK-PSAASIDA----
                                                                                                                                                                                           -----TDGSGTA-LGWTVAWKNNYRNAHSATTWSGQYVGGAEARINTQWLLTSGTTEA 141
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Pred. No. 6.9;
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                                                                                                               ----AKKAGV-----NNGN 176
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A; Residues: 1-741 <COL>
A; Cross-references: GB: Z78020; GB: AL123456; NID: g3261625; PIDN: CAB01465.1; PID: e25767
A; Experimental source: strain H37Rv
C; Genetics:
A; Gene: g1cB
                                                                                                                                                                                                                                                                                                                                                         Qy
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70500; MUID:98295987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable glcB protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Uul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: F70722
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275 SVAAVDAADKVLGYRNWLGLNKGDLAAAVDK 305
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                                           SAASIDAAKKA-----GVNNGNPLDAVQQ 183
                                                                                                                                            PTYNKVRGDKVIAYARKFLDDSVPLSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQF 217
                                                                                                                                                                                                                                               -TYESAVGNAESRYVLTGRYDSAPATDGS-GTALGWT-----VAWKNNYRNAHSATTW 116
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Search completed: April 6, 2001, 00:17:14 Job time: 10899 sec

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Result
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"Structural studies of binding site tryptophan mutants in the high-affinity streptavidin-biotin complex.";
J. Mol. Biol. 279:211-221(1998).
-!- FUNCTION: THE BIOLOGICAL FUNCTION OF STREPTAVIDIN IS NOT KNOWN.
FORMS A STRONG NON-COVALENT SPECIFIC COMPLEX WITH BIOTIN (ONE MOLECULE OF BIOTIN PER SUBUNIT OF STREPTAVIDIN).
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SUBUNIT: HOMOTETRAMER.
SUBCELLULAR LOCATION: SECRETED.
SIMILARITY: BELONGS TO THE AVIDIN/STREPTAVIDIN FAMILY.
DATABASE: NAME-Prozyme technical fact sheet;
  DATABASE: NAME=ProZyme technical fact sheet; www-ntp://www.prozyme.com/technical/salOdata.html".
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15-OCT 94

15-OCT 94

01-NOV 97

15-MAY 97

15-MAY 97

13-APR 96

03-APR 96

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1- FUNCTION: THE BIOLOGICAL FUNCTION OF STREPTAVIDIN IS NOT FORMS A STRONK NON-COVALENT SPECIFIC COMPLEX WITH BIOTIN MOLECULE OF BIOTIN PER SUBUNIT OF STREPTAVIDIN).

1- SUBURIT: HOMOTETRAMER (BY SIMILARITY).

1- SUBCELLULAR LOCATION: SECRETED.

1- SIMILARITY: BELONGS TO THE AVIDIN/STREPTAVIDIN FAMILY.
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m Adar R., Wilchek
                                                                                                                                                                                                                                                                                                                                              AVIDIN;
                                                                                                                                         132
                                                                                                                                                                                 116
                                                                                                  144
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183
67
                                                              18864
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  99
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ng streptavidin-like,
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                                                            ₹
  Score 932;
                                                                             SIMILARITY)
                                                                                                                                                                             SIMILARITY).
INVOLVED IN BIOTIN
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STREPTAVIDIN V1.
INVOLVED IN BIOTIN
                                                                                                                                                                                                                                         SIMILARITY).
                                                                                                                         SIMILARITY
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<u>بر</u>
                                                                                                                                                                                                                                                            BINDING
                                                            CRC64;
                                                                                                                                         BINDING
                                                                                                                                                                                                                       BINDING
Length 183;
                                                                                                                                                                                 BINDING
                                                                                                  BINDING
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RESULT
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Matches 182; Conservative
                                                                                                                                                                                                                                                                                                      From Streptomyces.";

Biochim. Biophys. Acta 1263:60-66(1995).

FORMING A STRONG NON-COVALENT SPECIFIC COMPLEX WITH BIOT:

FORMS A STRONG NON-COVALENT SPECIFIC COMPLEX WITH BIOT:

MOLECULE OF BIOTIN PER SUBUNIT OF STREPTAVIDIN).

SUBUNIT: HOMOTETRAMER (BY STANLARITY).

SUBUNIT: HOMOTETRAMER (BY STANLARITY).
                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREPTAVIDIN VA FRECURSON, VI. STREPTAVIDIN VA FRECURSON, Streptomyces violaceus (Streptomyces venezuelae).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
SEQUENCE
                     BINDING
                                                                                                                                                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
STREPTAVIDIN V2 PRECURSOR (SA V2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q53533;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _STRVL
                                                                                      BINDING
                                                                                                                               SIGNAL
                                                                                                                                               PFAM; PF01382; Avidin; PROSITE; PS00577; AVIDIT
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95359204; PubMed-7632734;
Bayer E.A., Kulik T., Adar R., Wilchek M.;
"Close similarity among streptavidin-like,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAV2_STRVL
                                                                                                          BINDING
                                                                                                                                                                                    EMBL; S78782;
HSSP; P22629;
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=95359204;
                                                                                                                                            Signal;
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183 AA;
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STREPTAVIDIN V2.
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SIMILARITY).
INVOLVED IN BIOTIN E
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0; Mismatches
          SIMILARITY)
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                                                    SIMILARITY)
                                                                          SIMILARITY)
                     INVOLVED IN BIOTIN
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1;
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                                                               BIOTIN
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                                                                                                                                                                                                                                                                                                                                                                                                 biotin-binding proteins
CRC64;
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RESULT 4
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ID AVR4_C
AC P56734
DT 30-MAY
DT 10-CIN
GALLus
RN GALLus
RN FINAL
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                        Query Match
Best Local
    Matches
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Best Local S
                                                                                                           CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                        INTERPRO; IPKOVVVI
PRINTS; PROO709; AVIDIN.
PROSITE; PSO0577; AVIDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVR4_CHICK P56734;
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                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                    Biotin; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Toimela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94170814; PubMed=8125122
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30-MAY-2000 (Rel. 39, Last sequence up
01-CCT-2000 (Rel. 40, Last annotation
AVIDIN-RELATED PROTEIN 4/5 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel.
30-MAY-2000 (Rel.
01-OCT-2000 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular cloning
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                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE AVIDIN/STREPTAVIDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND AVR5 ARE IDENTICAL.
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                                                                                                                                                                                                                                                                                                                   Z22883; -; NOT_ANNOTATED_CDS
    45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T.A., Helenius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                       141
150
    Conservative
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93
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                                                                                                           AA;
                                                                                                                                                                                                                                    Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wallen M.J., Kristo P.A., Laukkanen M. elenius M.A., Kulomaa M.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                            AVIDIN;
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Neognathae; Galliformes; Phasianidae; Phasiani
                        15.7%;
33.8%;
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95.1%;
                                                                                                           MW;
                                                                                                                                                                                                                                                        FALSE_NEG
                                                                                                                                                                                                                                    family
    22;
Score 146.5;
Pred. No. 1.8e
22; Mismatches
                                                                                                  N-LINKED (GLCNAC. ...) (PO
N-LINKED (GLCNAC. ...) (PO
N-LINKED (GLCNAC. ...) (PO
; 9A6C6C6310EFE13A CRC64;
                                                                                                                                                                                          POTENTIAL.
AVIDIN-RELATED
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Pred. No. 3
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.9e-66;
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                                       DB 1;
                                                                                                                                                                PROTEIN 4/5.

AC. . .) (POTENTIAL).
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                                         Length
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                                                                                                                          (POTENTIAL)
                                         150;
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  19;
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GN AVID.
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RA GOPE |
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RA CHANG
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RP SEQUE
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RI [4]
RP SEQUE
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RY MEDLII
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21-JUL-1986 (Rel. 0
01-NOV-1991 (Rel. 2
30-MAY-2000 (Rel. 3
                                                                                                                                                                                                                           IMPORTANCE OF TYR IN BIOTIN-BINDING. MEDLINB-90351377; PubMed-2386489; Gitlin G., Bayer E.A., wilchek M.; "Studies on the biotin-binding sites c Tyrosine residues are involved in the Biochem. J. 269:527-530(1990).
                                                                                                                                                                                                                                                                                                                                                                                                    Delange R.J., Huang T.-S.; "Egg white avidin. 3. Sequence of the 78-residue middle cyanogen control complete amino acid sequence of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic
[2]
                         MEDLINE=93281699;
                                                                                                                                                                                                                                                                                                                                                                                           bromide peptide. Complete amino acid subunit.";
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      Livnah O.,
                                          X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
                                                                                                                                                                                       BIOTIN-BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 25-152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wallen M.J., Laukkanen M.O., Kulomaa M.S.;
"Cloning and sequencing of the chicken egg-white avidin-encoding gene and its relationship with the avidin-related genes Avrl-Avr5.";
Gene 161:205-209(1995).
                                                                                                                                                                  MEDLINE=91378911; PubMed=1898347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=71107558; PubMed=5100763;
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                                                                                                                             "Studies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Cloning and expression of avidin in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chandra G., Gray J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=90355928;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular cloning
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Zarucki-Schulz T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=87203384; PubMed=3575102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
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                                                                                                      , Bayer E.A., Wilchek M.;
on the biotin-binding site
biotin.";
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    Bayer E.A.,
                                                                                   278:573-585(1991).
                                                                                                                                                                                       STUDIES
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                         PubMed=8506353;

    Last sequence update)
    Last annotation update)

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Neognathae; Galliformes; Phasianidae; Phasianinae;
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    Wilchek M.,
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    Sussman J.L.;
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he binding s
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Three-dimensional structures of avidin and the avidin-biotin

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EMBL; X05343; CAA28954.1; -.
EMBL; L27818; AAB59733.1; -.
PIR; A03160; VICH.
PIR; A27518; A27518.
PIR; S11540; S11540.
PDB; 2AVI; 15-JUL-93.
PDB; 1AVD; 31-JAN-94.
PDB; 1AVD; 31-JAN-94.
PDB; 1AVD; 31-JUL-98.
PDB; 1AVV; 15-JUL-98.
PDB; 1AVV; 15-JUL-98.
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CARBOHYD
BINDING
VARIANT
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                                                                                          TURN
STRAND
                                                                                                                                                                                                                                                  PFAM; PF01382; Avidin; 1.
PRINTS; PR00709; AVIDIN.
PROSITE; PS00577; AVIDIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nardone E., Rosano C., Santambrogio P., Siccardi A.G., Paganelli G., Losso R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pugliese L., Coda A., Malcovati M., Bolognesi M.;
"Three-dimensional structure of the tetragonal crystal
egg-white avidin in its functional complex with biotin
                                                                                                                                                                                                                         Glycoprotein;
SIGNAL
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Eur. J. Biochem. 256:453-460(1998)
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                                                                                                                                                                                                                                                                                          INTERPRO; IPR000088; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Blochemical characterization and crystal structure of a recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 90:5076-5080(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOTIN FEW CONCENT SUBUNIT: HOMOTETRAMER.

SUBUNIT: HOMOTETRAMER.

TISSUE SPECIFICITY: SYNTHESIZED IN HEN OVIDUCT AND CONCENT EGG WHITE (WHERE IT REPRESENT 0.05% OF THE TOTAL PROTEIN).

SIMILARITY: BELONGS TO THE AVIDIN/STREPRAVIDIN FAMILY.

DATABASE: NAME-Worthington enzyme manual;

WWW-"http://www.worthington-biochem.com/manual/a/av.html".

DATABASE: NAME-Prozyme technical fact sheet;

WWW-"http://www.prozyme.com/technical/avlodata.html".

WWW-"http://www.prozyme.com/technical/avlodata.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Biol. 231:698-710(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . J. Biochem. 256:453-460(1998).
FUNCTION: THE BIOLOGICAL FUNCTION OF AVIDIN IS NOT KNOWN. FORMS STRONG NON-COVALENT SPECIFIC COMPLEX WITH BIOTIN (ONE MOLECULE OF BIOTIN PER SUBUNIT OF AVIDIN).
Signal;
41
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222
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74
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                                                                                                                               N-LINKED (GLCNAC. . .).
INVOLVED IN BIOTIN BINDING.
I -> T (IN APPROX. 50% OF THE CHAINS).
G -> S (IN REF. 3).
E -> Q (IN REF. 2 AND 3).
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34 VSAAEAGITGTWYNQLGSTFIVTAGA---DGALTGTYESAV---

25;

Mismatches

42;

Indels

23;

Gaps

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P56735;
30-MAY-2000
30-MAY-2000
01-OCT-2000
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HELIX
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SEQUENCE
                                                                               CARBOHYD
CARBOHYD
                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; (
Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
01-OCT-2000 (Rel. 40, Last annotation
01-OCT-2000 (Rel. 40, Last annotation
                                                                                                                 Biotin; Signal;
SIGNAL
                                                                                                                                                                                                                                                                                                                                             STRAIN=RHODE ISLAND;
Ahlroth M.K., Kola E.H., Ewald D., Masabanda J., Sazanov A., Fries Kulomaa M.S.;
                                                          SEQUENCE
                                                                     CARBOHYD
                                                                                                        CHAIN
                                                                                                                                       PRINTS; PR00709; AVIDIN. PROSITE; PS00577; AVIDIN;
                                                                                                                                                               EMBL; AJ237658; CAB39893.1; INTERPRO; IPRO00088; -
                                                                                                                                                                                                                                                                                             Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                          "Characterization and 
gene family.":
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 33.0
Similarity 32.4
44; Conservative
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130
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152
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141
150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                               Multigene
                                                                               24
150
54
93
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135
146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16769 MW;
        13.3%;
                                                          16528
                                                                                                                                                                                                                                                                                                                                  chromosomal localization
                                                                                                                               1.
family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 143.5; DB 1
Pred. No. 3.2e-05
                                                       POTENTIAL.

AVIDIN-RELATED PROTEIN 6.

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

COF3357D6291B150 CRC64;
         Score 124.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1D55A4491D5EFD5C CRC64;
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           0.0011;
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                    Length
                                                                                                                                                                                                                                                                                                                                   chicken
                                                                                                                                                                                                                                                                                                                                                                                                                      Phasianinae;
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                                                                                                                                                                                                                                                                                                                                  avidin
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                                                                                              Query Match
Best Local S
Matches 44
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CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVR1_CHICK STANDARD; PRT; 150 AA. 013153; 15-JUL-1999 (Rel. 38, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                          Biotin; Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z21611; -; NOT_ANNOTATED_CDS.
EMBL; Z97063; CAB09798.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHICK
                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00709; AVIDIN.
PROSITE; PS00577; AVIDIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eur. J. Biochem. 220:615-621(1994).
-!- SIMILARITY: BELONGS TO THE AVIDIN/STREPTAVIDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Keinaenen R.A., Wallen M.J., Kristo P.A., Laukkanen M.O., Toimela T.A., Helenius M.A., Kulomaa M.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-WHITE LEGHORN; TISSUE-OVIDUCT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVIDIN-RELATED PROTEIN 1 PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                INTERPRO; IPRO00088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94170814; PubMed=8125122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Keinaenen R.A., Laukkanen M.-L., Kulomaa "Molecular cloning of three structurally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=88260103; PubMed=2838690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-OVIDUCT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular cloning and nucleotide sequence of chicken avidin-related

    Steroid Biochem.

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                                         VSAAEAGITGTWYNQLGSTFIVTAGA---DGALTGTYESAV----GNAESRYVLTGRYDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biochem.
{\tt LSARKCSLTGKWDNDLGS--IMTIGAVNDNGEFNGTYITAVADNPGNITRSPLLGIQHKR}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DWKATRVGYNNFTR 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AWKSTLVGHDTFTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APATDGSGTALGWTVAWKNNYRNAHSATTWSGQ-YV--GGAEARINTQWLLTSGTTE-AN 142
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                                                                                              Similarity 32.4
44; Conservative
                                                                                                                                                                                                                                                                                                                                                          lgnal;
                                                                                                                                                                                                                150
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67
93
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                                                                                                                                                                                                                                                                                                                                                          Multigene
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                                                                                                                    13.0%;
                                                                                                                                                                                                                                                                                                                                                          1.
family.
                                                                                                                                                                                                                WW.
                                                                                              24;
                                                                                            Score 121.5;
Pred. No. 0.00
24; Mismatches
                                                                                                                                                                                                                              AVIDIN-RELATED PROTEIN 1.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
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                                                                                                                    , DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               related
                                                                                              43;
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                                                                                            23;
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Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ULT 8
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene family.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE AVIDIN/STREPTAVIDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biotin; Signal; Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00709; AVIDIN. PROSITE; PS00577; AVIDIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ237659; CAB39894.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kulomaa M.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=RHODE ISLAND;
Ahlroth M.K., Kola E.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken).
                                                                    145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Characterization and chromosomal localization of the chicken
133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 DWKATRVGNNDFTR 144
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                                                                KSTLVGHDTFTK 156
KATRVGYNNFTR
                                                                                                                                                                                                        ATDGSGTALGWTVAWKNNYRNAHSATTWSGQYV----GGAEARINTQWLLTSGTTE-ANAW 144
                                                                                                                                                                                                                                                                         LSARKCSLTGEWDNNLGSNMTIGAVNDNGEFNGTYITAVADNPGNIKLSPLLGIQHKRA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AWKSTLVGHDTFTK
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                                                                                                                                    CQPTFGFTVHW--NF--SESTSVFVGQCFIDRSGKEV-LKTKWLQRLAVDDISDDW
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150 AA;
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144
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41
54
93
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Neognathae; Galliformes; Phasianidae; Phasiani
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e family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 121.5;
Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.

AVIDIN-RELATED PROTEIN 7.
                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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RESULT 9 AVR3\_CHICK

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Best Local S
Matches 40
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R EMBL; Z21536; -; NOT_ANNOTATED_CDS.

RIVTERPRO; IPRO00088; -;
R PRINTS; PR00709; AVIDIN.

R PROSITE; PS00577; AVIDIN; 1.

R POTENTIAL.

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"FBP1_STRPU
FFB079;
01-MAR-1989
01-FEB-1996
30-MAY-2000
FIBROPELLIN
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P56733;
30-MAY-2000
30-MAY-2000
01-OCT-2000
(UEGF-1).

(UEGF-1).

Strongylocentrotus purpuratus (Purple sea urchin).

Strongylocentrotus purpuratus (Eleutherozoa; Echinozoa; Echinozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a copyright the EMBL the European Bioinformatics institute. The European Bioinformatics institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genes
Eur.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Keinaenen R.A., Wallen M.J., Kristo P.A., Laukkanen M.O.,
Tolmela T.A., Helenius M.A., Kulomaa M.S.;
"Molecular cloning and nucleotide sequence of chicken avidin-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archosauria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVIDIN-RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94170814; PubMed=8125122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATDGSGTALGWTVAWKNNYRNAHSATTWSGQYV----GGAEARINTQWLLTSGTTE-ANAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSARKCSLTGKWTNNLGSIMTIRAVNSRGEFAGTYLTAVADNPGNIKLSPLLGIQHKRA-81
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                                                                                                                                                                                                                                                                                                                                                                                         KSTLVGHDTFTK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   CQPTFGFTVHW--NF--SESTSVFVGQCFIDRSGKEV-LKTKWLQRLAVDDISDDW
                                                                                                                ) (Rel. 10, Cr.
5 (Rel. 33, La.
) (Rel. 39, La.
N I PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Metazoa;
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(Rel. 39, Last sequence up
(Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220:615-621(1994)
                                                                                                                10, Created)
33, Last sequence update)
39, Last annotation updat
CURSOR (EPIDERMAL GROWTH F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 120.5; DB Pred. No. 0.0023 4; Mismatches '
                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                  GROWTH FAC
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on update)
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(See http://www.isb-sib.ch/announce/
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INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO;

| IPRO00088; -. | IPRO00152; -. | IPRO00561; -. | IPRO00859; -. | IPRO01438; -. | IPRO01881; -. | | | IPRO01881; -. | | | IPRO01881; -. | | | IPRO01881; -. | | | IPRO01881; -. | | | | | | | | | | | | | |

EMBL; EMBL; EMBL; PIR; /

3L; L08692; AAA62164.1; L08692; AAA62163.1; L317530; CAA35571.1; L31, X17530; CAA35573.1; L4, X17533; CAA35573.1; L4, X17533; CAA35573.1; L4, A29316; A29316;

HSSP;

EMBL;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDINE-90112459; PubMed-2514273; MEDINE-90112459; PubMed-2514273; Delgadillo-Reynoso M.G., Rollo D.R., Hursh D.A., Raff "Structural analysis of the uegene in the sea urchi strongylocentrotus purpuratus reveals more similarity than to invertebrate genes with EGF-like repeats."; J. Mol. Evol. 29:314-327(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A sea urchin gene encodes a polypeptide growth factor.", Science 237:1487-1490(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dev.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bisgrove B.W., Andrews M.E., Raff R.A.; "Fibropellins, products of an EGF repeat-containing unique extracellular matrix structure that surrounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 279-476 AND 781-1064 FROM MEDLINE-87319677; PubMed-3498216; Hursh D.A., Andrews M.E., Raff R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   embryo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-91285254; PubMed-2060714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FASEB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-89196806; PubMed-2784773; Hunt L.T., Barker W.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERIZATION
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                                                                                                                                                                                                                     AND ZYGOTICALLY.

SIMILARITY: CONTAINS 21 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 1 CUB DOMAIN.
SIMILARITY: THE C-TERMINAL DOMAIN OF THIS
TO AVIDIN/STREPTAVIDIN.
                                                                                                                                                                                                                                                                                                                                                   DURING EARLY CLEAVAGE, THEN RAPIDLY INCREASES IN ABUNDANCE BETWEEN LATE MORULA AND MESENCHYME BLASTULA STAGES TO MAXIMAL LEVELS MAINTAINED THROUGH SUBSEQUENT STAGES. EXPRESSED FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MATRIX.

SUBCELLULAR LOCATION: EXTRACELLULAR. IN VESICLES IN THE CYTOPLAS SUBCELLULAR LOCATION: EXTRACELLULAR. IN VESICLES IN THE CYTOPLAS OF UNFERTILIZED EGGS, THEN TO THE BASE OF THE HYALIN LAYER THROUGHOUT DEVELOPMENT AND FINALLY IN THE APICAL LAMINA IN LATE EMBRYOS AND EARLY LARVAE.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; IA (SHOWN HERE) AND IB; ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALTERNATIVE PRODUCTS: 2 ISOFORMS; IA (SHOWN HERE) PRODUCED BY ALTERNATIVE SPLICING. THE SMALL FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. 146:89-99(1991).
FUNCTION: FORM THE APICAL LAMINA, A COMPONENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. 3:1760-1764(1989).
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LAYER
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OR CREAR CARTAIN CARTA
Biotin; Altern
Glycoprotein.
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PROSITE;
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PS00022;
PS00577;
PS01180;
PS01186;
PS01187;
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EGF_1; 19.
AVIDIN; 1.
CUB; 1.
EGF_2; 19.
EGF_CA; 19.
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          splicing;
  EGF-LIKE 2, CLEGF-LIKE 3, CLEGF-LIKE 4, CLEGF-LIKE 6, CLEGF-LIKE 6, CLEGF-LIKE 10, CLEGF-LIKE 10, CLEGF-LIKE 11, CLEGF-LIKE 12, CLEGF-LIKE 11, CLEGF-LIKE 12, CLEGF-LIKE 13, CLEGF-LIKE 13
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  Y SIMILARITY
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RESULT 11

AVR2_CC
ID AVR2_CC
AC P56733
DT 30-MAY
DT 30-MAY
DT 30-MAY
DT AVIDIT
GN AVR2_C
OC Eukary
OC Archos
OC Gallus
CC Gallus
RN 11
RP SEQUEI
RC STRAII
RX MEDLII
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STRAIN-WHITE LEGHORN; TISSUE-OVIDUCT;

KEDLINE-94170814; PubMed-8125122;

Keinaenen R.A., Wallen M.J., Kristo P.A., Laukkanen M.O.,

Toimela T.A., Helenius M.A., Kulomaa M.S.;

"Molecular cloning and nucleotide sequence of chicken avic
genes 1-5.";

Eur. J. Biochem. 220:615-621(1994).

EIR. SIMILARITY: BELONGS TO THE AVIDIN/STREPTAVIDIN FAMILY.
                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken)..
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                AVR2_CHICK STANDARD; PRT; 150 AA. p56732; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) AVR2.
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Pred.
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No. 0.
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                                                                                    avidin-related
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Matches 44
                                                                                                                                                                                                                                                                                                   CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                  MEDLINE-89008089; PubMed-3049545; Fisher J.A., Smit J.K., Agabian N.; "Transcriptional analysis of the major
                                                                                                                                                                             Gilchrist A., Fisher J.A., Smit J.K.;
"Nucleotide sequence analysis of the gene encoding the Caulobacter crescentus paracrystalline surface layer protein.";
Can. J. Microbiol. 38:193-202(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0709; AVIDIN.
PROSITE; PS00577; AVIDIN; FALSE_NEG
Biotin; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z21554; -; NOT_ANNOTATED_CDS.
EMBL; Z21535; -; NOT_ANNOTATED_CDS.
INTERPRO; IPRO00088; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
            MEDLINE-98292737;
Awram P., Smit J.
                                        STRAIN-CB1
                                                                                         Caulobacter crescentus."
                                                                                                                                           SEQUENCE OF 1-313
STRAIN-ATCC 19089
                                                                                                                                                                                                                               STRAIN-ATCC 19089
MEDLINE-93007489;
                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                  CAUCR
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                                                    CHARACTERIZATION
                                                                            J. Bacteriol. 170:4706-4713(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 DWIATRVGNNDFTR 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 AWKSTLVGHDTFTK 156
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Caulobacter crescentus paracrystalline S-layer protein
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67
93
150 AA;
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                          PubMed=9620954;
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                                                                                                                                         FROM N.A.,
CB15;
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AVIDIN-RELATED PROTEIN 2.

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N-LINKED (GLCNAC. . .) (POT

N-LINKED (GLCNAC. . .) (POT
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Matches 54
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harri Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyc Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quali M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston Taylor K., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
PROBABLE MALATE SYMTHASE G (EC 4.1.3.2).
GLCB OR RV1837C OR MTCY1A11.06.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              secreted by an ABC transporter (type I) secretion apparatus.";

J. Bacteriol. 180:3062-3069(1998).

-I- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.

-I- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
S-LAYER WITH HEXAGONAL SYMMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell wall; S-layer; Calcium-binding INIT_MET 0 0 SEQUENCE 1025 AA; 98209 MW; AFC
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                                                                                                                                                                   STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                                                             Q50596;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                             MEDLINE-98295987; PubMed-9634230;
                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                 Actinomycetales; Corynebacterineae;
                                                                                                                                                                                                                                     Bacteria; Firmicutes; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                           MASZ_MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00353; hemolysinCabind; PRINTS; PR00313; CABNDNGRPT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VQAAAVTALPTGVTISGIETMNVTSGAAITLNTSSGVTGLTALNTNTSGAAQTVTAGAGQ 357
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Pred. No. 0.
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Mycobacteriaceae; Mycobacterium.
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Matches
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P47551; Q49317;
01-FEB-1996 (Rel. 3
01-FEB-1996 (Rel. 3
01-NOV-1997 (Rel. 3
                                                    Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M., Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L., Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M., Nguyen D.T., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.; "The minimal gene complement of Mycoplasma genitalium."; Science 270:397-403(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                        MYCGE
                                                                                                                                                                                                                                                                   Mycoplasma genitalium.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
STRAIN-ATCC
                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-ATCC 33530 / G-37;
MEDLINE-6026346; Pubmed=7569993;
                           SEQUENCE OF
                                                                                                                                                                                                                                                         Mycoplasmataceae;
                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TUBERCULIST; RV1837C; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z78020; CAB01465.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGQYVGGAEARINTQWLLTS----------GTTEANAWKSTLV--GHDTFTKVKP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 {\tt PTYNKVRGDKVIAYARKFLDDSVPLSSGSFGDATGFTVQDGQLVVALPDKSTGLANPGQF}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IAVSLTTVSITASASAD----PSKDSKAQVSAAEAGITGTWYNQLGSTFIVTAGADGALTG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -TYESAVGNAESRYVLTGRYDSAPATDGS-GTALGWT-----VAWKNNYRNAHSATTW 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             non-profit institutions as long as and this statement is not removed. U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               email to license@isb-sib.ch).
          1138-1224 FROM 33530 / G-37;
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                                                                                                                                                                                                                                                                                                                      (Rel. 33, Created)
(Rel. 35, Last sequence update)
(Rel. 35, Last annotation update)
LIPOPROTEIN MG309 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                         Mycoplasma
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Pred. No. 1.1;
28; Mismatches
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Best Local
  Science [2]
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EMBL; U02200;
TIGR; MG309; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
SEQUENCE
                                                                                                                       Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Maj
                                                                                                                                                                                                                                                                                                                                                             SIDE TAIL FIBSTER OR B1372
                                                                                                                                                                                                                                                                                                                                                                                                            P76072; P77560;
01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ECOLI
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                       "The complete genome sequence Science 277:1453-1474(1997).
                                                                          Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose
Mau B., Shao Y.;
                                                                                                                                                                           STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                     Escherichia.
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                                                                                                                                                                                                                                                                                                                                     Escherichia coli.
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J. Bacteriol.
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Peterson S.N., Hu P.-C., Bott K.F., Hutchison
"A survey of the Mycoplasma genitalium genome
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ical protein; Lipoprotein; Membrane; Signal.
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L -> V (IN REF. 2).
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                                                    of Escherichia coli K-12.";
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by using
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Matches 42
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Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
Alba H., Baba T., Fujita K., Hayashi K., Kitakawa M., Kitagawa M.,
Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
Nakade S., Nakamura Y., Nashimoto H., Nishito Y., Oshima T., Saito N.,
Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,
Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
Takomoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
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Takemoto K., Sirakeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
Takemoto K., Sirakeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
Takemoto K., Sirakeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
Takemoto K., Sirakeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
Takemoto K., Wada C., 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; Fiber protein; Repeat. SEQUENCE 1120 AA; 113779 MW; 542E59D71EE795B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE000234; AAC74454.1; ALT_INIT.
EMBL; D90774; BAA14966.1; -.
EMBL; D90775; BAA14975.1; -.
ECOGENE; EG13370; STFR.
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STRAIN-K12;
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INTERPRO; IPRO00122; -.
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                                                                                                                                                                                                                                                      129 NTQWLLTSGTTE--ANAWKSTLVGHDTFTKVKPSAASIDAAKKAGVNNGN 176
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nes 42; Conserv
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Pred. No. 4.2;
2; Mismatches 89; Indels 7;
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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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SPTREMBL_15:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungl:*
4: sp_human:*
5: sp_invertebrate
6: sp_manmal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_vortebrate
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936
1 MRKIVVAAIAVSLTTVSITA.....IDAAKKAGVNNGNPLDAVQQ 183
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Gapop 10.0 , Gapext 0.5
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sp_plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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sp_phage:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	ω	2	<b>~</b>	Result No.
92	94	94	94.5	94.5	97	97.5	98	98.5	99.5	100	100	100.5	101	104	105.5	110.5	112	114	Score
9.8	10.0	10.0	10.1	10.1	10.4	10.4	10.5	10.5	10.6	10.7	10.7	10.7	10.8	11.1	11.3	11.8	12.0	12.2	Query Match Length
865	967	570	3381	507	443	729	595	832	1477	565	560	1026	595	595	1001	892	595	529	
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Q43919	Q08294	Q59665	Q9KX33	050506	Q28243	Q9KH34	Q9S0U1	054356	Q48028	Q9S4M4	Q9S4M2	Q9RFI2	Q06351	Q9S0T7	Q05164	Q9KX38	Q06353	Q25058	Ī
Q43919 aeromonas c	Q08294 saccharomyc	Q59665 pseudomonas	Q9kx33 streptococc	O50506 streptomyce	Q28243 canis famil	Q9kh34 antarctic b	Q9s0ul escherichia	O54356 moraxella c	Q48028 haemophilus	Q9s4m4 escherichia	Q9s4m2 escherichia	Q9rfi2 caulobacter	Q06351 escherichia	Q9s0t7 escherichia	Q05164 saccharomyc	Q9kx38 moraxella c	Q06353 escherichia	Q25058 heliocidari	Description

45	44	43	42	41	40	39	38	37	36	35	34	3 3	32	31	30	29	28	27	26	25	24	23	22	21	20
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9.3	•						9.5						•	•	9.7	9.7	9.7	•	9.7	•	•	•	•	•	9.8
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P95620	Q9RPY6	Q9U6M5	Q9LAQ7	Q9L962	Q52657	P95586	039781	Q45977	018758	Q9RQB7	Q9L960	Q19522	Q9KWR3	Q9LAR0	Q9LAR1	Q9S0T5	Q53789	039782	030678	Q9XCK3	P95642	Q9Z1U3	P96141	Q9L964	Q17240
P95620 rickettsia	Q9rpy6 campylobact	Q9u6m5 globodera t	Q9laq7 rickettsia	Q91962 moraxella c	Q52657 rickettsia	P95586 rickettsia	039781 equine herp	Q45977 caulobacter		_	_	Q19522 caenorhabd1	Q9kwr3 streptococc	_	Q9lar1 rickettsia	Q9s0t5 escherichia	Q53789 shigella bo	039782 equine herp	O30678 xanthomonas	Q9xck3 streptococc	P95642 rickettsia	Q9zlu3 rickettsia	thai tick	Q91964 moraxella c	Q17240 bombyx mori

## ALIGNMENTS

DR DR	DR DR	묘묘묘	D DR	Z Z Z	DR DR	DR DR	DR CR	D R	RA	R P	28	38	88	2 2	D D	DT	8 B	RESULT Q25058
PROSITE; PS00103; ASX_HYDROXYL; UNKNOWN_8.  PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_11.  PROSITE; PS00027; EGF_1; UNKNOWN_11.  PROSITE; PS00577; AVIDIN; 1.  PROSITE; PS01186; EGF_2; 10.  PROSITE; PS01187; EGF_CA; 7.	; PR00012; ; PR00286; ; PR00287;	PEAM; PEOUDO, ESE, IO. PEAM; PEO1382; AVIDIN; 1. PRINTS; PROUOLO; ESFBLOOD. PRINTS; PROUOL1; ESFLAMININ.	PRO; IPR001947; PRO; IPR002049;	INTERPRO; IPRO01010; INTERPRO; IPRO01438; INTERPRO; IPRO01881: -		INTERPRO; IPRO00088; INTERPRO; IPRO00152;	INTERPRO; IPRO00083;	L33861;	ATIN-1005) to the EMBI (Condant /DDBT	[1] SEOUENCE FROM N.A.	NCBI_TaxID=7634;	Euechinoidea; Echinacea; Echinoida; E	Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;	IA (FRAGMENT).		(TrEMBLrel. 01, Creat	Q25058 PRELIMINARY; PRT; 529 AA.  Q25058;	058 1

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STRAIN-BI 316-42 / SEROTYPE 09:K9:H12;

MEDLINE-9337483; PubMed-8366026;

Schoenhals G., Whitfield C.;

"Comparative analysis of flagellin sequences from Escherichia coli
strains possessing serologically distinct flagellar filaments with a
shared complex surface pattern.";

J. Bacteriol. 175:5395-5402(1993).

-i- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO
FORM THE FILAMENTS OF BACTERIAL FLAGELLA.

EMBL; L07389; AAA23799.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Protec
Escherichia.
NCBI_TaxID=562;
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Q06353;
Q1-NOV-1996
Q1-NOV-1996
Q1-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00207; PRODOM; PD000316;
462 NNGKYTYDSGTGTGKYAPKYGAEYYYSANGTLTTDATSEGTYTKDPLKALDEAISSIDKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERPRO; IPR001029; -.
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                                         105 NNYRNAHSATTWSGQYVG--GAEARINTQWLLTS-GTTEANAWKSTLVGHD----TFTKV 157
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                                                                                            TITYKSGVQTYQAVFAAGDGTASAKYADKADVSNATATYTDADGEMTTIGSYTTKYSIDA
                                                                                                                                                                                    ASVIMGGITINFKTGADAD-AATANAGVSFIDTASKETVLNKVATAKQGKAVAADGDISA 401
                                                                                                                                                                                                                                AAIAVSLTTVSITASASADPSKDSKAQVSAAEAGITGTWYNQLGST---FIVTAGADGAL 63
                                                                                                                                               TGTYESAV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAWKSTLVGHDTFTKVKPSAA 162
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40; Conserv
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26.1%;
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                                                                                                                                           -GNAESRYVLTGRYDSAPAT----DGSGTALG-WTVAWK---
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01,
14,
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Last annotation update)
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                                                                                                                                                                                                                                                                                                           Score 112;
Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                        88510CD561EF25F9 CRC64;
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RESULT QUESTION AC QUESTION OCCUPANT OC
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Best Local Similarity
Matches 43; Conserv
                                                                                                                                                                Q05164 PRELIMINARY; PRT; 1001 AA. Q05164; Q05164; O1-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-AUG-1998 (TrEMBLrel. 07, Last annotation updat AOB567, AOF1001, AOE110, AOE264 AND AOE130 GENES. AOF1001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9KX38;
01-OCT-2000
01-OCT-2000
01-OCT-2000
  SEQUENCE FROM N.A. STRAIN=FY1679;
                                                                                              Saccharomycetaceae;
                                                                                                                  Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maciver I., Latimer J.L., Cope L.D., Thomas S.E., Hanses Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases EMBL; U61725, Aar36416.; . . SEQUENCE 892 AA; 93358 MW; 9D71A369672F44C7 CRC64;
                                                                        NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adherence Vitro.";
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Bacteria;
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MEDLINE=20138164; PubMed=10671460;
MEDLINE=20138164; PubMed=10671460;
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Adherence of Moraxella
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                                                                                            Saccharomyces.
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21.7%;
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Pred. No. 0.59
26; Mismatches
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Best Local S
Matches 51
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Best Local S
Matches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-1999) to the EMBI EMBL; AB028475; BAA85084.1; -. INTERPRO; IPRO01029; -. INTERPRO; IPRO01492; -. INTERPRO; IPRO01492; -. INTERPRO; IPRO01492; -. INTERPRO; IPRO01669; Flagellin_C; 1. PFAM; PF00700; Flagellin_C; 1. PFAM; PF00700; FLAGELLIN SEQUENCE 595 AA; 61020 MW; 8
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Q9SOT7;
Q9SOT7;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BI 316-42;
Ohnishi K., Ishioka K.,
"Cloning of H antigen ge
E.coli K-12.";
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Bacteria; Proteol
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nes 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                             KPSAASIDAAKKAGVNNGN 176
                                                                                                                                                                                         TITYKSGVQTYQAVFAAGDGTASAKYADKADVSNATATYTDADGEMTTIGSYTTKYSIDA
                                                                                                                                                                                                                                           TGTYESAV-----
                                                                                                                                                                                                                                                                                        ASVTMGGTTYNFKTGADAD-AATANAGVSFTDTASKETVLNKVATAKQGKAVAADGDTSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSSSLTELTSSSTEVSSSIAPSTSS----SEVSSSITSSGSSVSGSSSITSSGSSVSSSS 118
RSSLGAIQNRLDSAVTNLN
                                                                                          NIGKVTVDSGTGTGKYAPKVGAEVYVSANGTLTTDATSEGTVTKDPLKALDEAISSIDKF
                                                                                                                                         NNYRNAHSATTWSGQYVG--GAEARINTQWLLTS-GTTEANAWKSTLVGHD----TFTKV
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                                                                                                                                                                                                                                                                                                                                                                                          51,
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                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                         11.1%; 25.6%;
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24.7%;
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13,
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                         Score 104;
Pred. No. 1
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Pred. No. 1.7
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                                                                                                                                                                                                                                                                                                                                                                                     88;
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Best Local S
Matches 51
                                                                                                                                                            Q9RFI2 PRELIMINARY;
Q9RFI2;
01-MAY-2000 (TrEMBLrel. 13, C
01-MAY-2000 (TrEMBLrel. 13, I
01-JUN-2000 (TrEMBLrel. 14, I
S-LAYER PROTEIN.
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Q06351;
Q1-NOV-1996
Q1-NOV-1996
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SEQUENCE
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J. Bacteriol. 175:5395-5402(1993).
i- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO FORM THE FILAMENTS OF BACTERIAL FLAGELLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schoenhals G., Whitfield C.; "Comparative analysis of flagellin sequences from Escherichia colistrains possessing serologically distinct flagellar filaments with
                                                                                                                   Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SIMILARITY: TO OTHER BACTERIAL EMBL; L07387; AAA23797.1; -INTERPRO, IPRO01029; -INTERPRO; IPRO01492; -
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Escherichia
  SEQUENCE FROM N.A.
                                            NCBI_TaxID=76;
                                                                         Caulobacter
                                                                                             Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00207; FLAGELLIN. PRODOM; PD000316; -; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-SU 1242 / SEROTYPE 01:K2:H1;
MEDLINE-93374833; PubMed-8366026;
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                                                                                          Proteobacteria; alpha
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                                                                                          subdivision;
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                                                                                          Caulobacter group;
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Q9S4M2;
01-MAY-2000 (TIEMBLIEL 1
01-MAY-2000 (TIEMBLIEL 1
01-CCT-2000 (TIEMBLIEL 1
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PFAM; PF00353; hemolyginCabind; 1.
PRINTS; PR00313; CABNDNGRPT.
PROSITE; PS00123; ALKALINE_PHOSPHATASE; UNKNOWN_1
SEQUENCE 1026 AA; 98132 MW; AD7DB818D7C528AC
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"The Secretion Signal of C. crescentus S-layer Protein is
the C-terminal 82 Amino Acids of the Molecule.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF193063; AAF19365.1; -.
                                                                                                                                                                                PFAM; PF00669; Flagellin_N; 1
PFAM; PF00700; Flagellin_C; 1
PRINTS; PR00207; FLAGELLIN.
PRINTS; PR00301; HEATSHOCK70.
PRINTS; PR00455; HTHTETR.
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EMBL; AF128954; AAD28525.2; -.
INTERPRO; IPRO01023; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99084952; PubMed=9864325;
Reid S.D., Selander R.K., Whittam T.S.;
"Sequence diversity of flagellin (flic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-E74/68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; P:
Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FLAGELLIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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IPR001647;
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Last annotation updat
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                   Score 100; DB Pred. No. 2.4;
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Pred. No. 4.2;
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                                                                                                                97DF005C9E0ABB71
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                                                                                                                   CRC64;
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                                         Length 560;
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O9S4M4;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
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J. Bacteria
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Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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PFAM; PF00700; Flagellin_C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERPRO; IPRO01029; -.
INTERPRO; IPRO01492; -.
INTERPRO; IPRO01647; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERPRO; IPRO01023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Bacteriol. 181:153-160(1
EMBL; AF128952; AAD28523.2;
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  158
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                                                                                                                                                                TGTYESAV------GNAESRYVLTGRYDSAPAT----DGSGTALG-WTVAWK---
KPSAASIDAAKKAGVNNGN 176
                                               NNGKYTYDSGTGTGKYAPKYGAEVYYSANGTLTTDATSEGTYTKDPLKALDEAISSIDKF
                                                                       NNYRNAHSATTWSGQYVG--GAEARINTQWLLTS-GTTEANAWKSTLVGHD----TFTKV 157
                                                                                                                                      TITYKSGVQTYQAVFAAGDGTASAKYADKADVSNATATYTDADGEMTTIGSYTTKYSIDA
                                                                                                                                                                                                                                 ASVTMGGTTYNFKTGADAD-AATANAGVSFTDTASKETVLNKVATAKQGKAAAADGDTSA 386
                                                                                                                                                                                                                                                                          AAIAVSLTTVSITASASADPSKDSKAQVSAAEAGITGTWYNQLGST---FIVTAGADGAL
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                                                                                                                                                                                                                                                                                                                       th 10.7%; Similarity 25.1%; So; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PR00207; FLAGELLIN.
PR00301; HEATSHOCK70.
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565 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        565
57857 MW;
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Pred. No. 2.4;
30; Mismatches
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Last annotation update)
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CS MOTAXE
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Q48028;
01-NOV-1996
01-NOV-1996
01-MAY-2000
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MEDLINE=92192797; PubMed=1548058;
Berenkamp S.J., Leininger E.;
Berenkamp S.J., Leininger E.;
"Cloning, expression, and DNA sequence analysis of genes nontypeable Haemophilus influenzae high-molecular-weight nontypeable related to filamentous hemagglutinin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
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HMW2A.
 MEDLINE=98013056; PubMed=9353007; Aebi C., Maciver I., Latimer J.L., Cope Thomas S.E., McCracken G.H. Jr., Hansen
                                                                                                                                                                                                                                                    1350
                                                                                                                                                                                                                                                                                                    1296
                                                                                                                                                                                                                                                                                                                                                                                                    1177
                                                                                    Moraxella catarrhalis.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                   1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Infect. Immun. 60:1302-1313(1992).
EMBL; U08875; AAA20524.1; -.
INTERPRO; IPR000169; -.
INTERPRO; IPR001000; -.
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NCBI_TaxID=727;
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                                                SEQUENCE FROM N.A.
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                                                                         NCBI_TaxID=480;
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CT-2000 (TrEMBLrel. 15,
CT-2000 (TrEMBLrel. 15,
MOLECULAR WEIGHT OUTER
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                                                                                                                                                                                                                                                                                                  TLTTVAGSDIK-----ATSGTLVINAKDAKLNGDASGDSTEVNAVNASGSGSVTAATSS 1349
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                                                                                                                                                                                                                                                                                                                        SCQYVCGAEARINTQWLLTSGTTEANAWKSTLVGHDTFTKVKPSA-----ASIDAAKKA 170
                                                                                                                                                                                                                                                                                                                                                                          YESAVGNAESRYVLTGRYDSAPATDGSG----TALGWTVAWKNNYRNAHSATTW 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
1477 AA; 154472 MW; B057C23F1AD24B0E CRC64;
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MEMBRANE PROTEIN.
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Pred. No. 7.6;
26; Mismatches
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Last sequence up
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              Stevens
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f Bordetella
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Best Local
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09S0U1;
01-MAY-2000
01-MAY-2000
01-JUN-2000
                                                                                                                                                 Ohnishi k., Ishioka K. "Cloning of H antigen E.coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; UNKNOWN_1.
SEQUENCE 832 AA; 88292 MW; 5C47F4F273350F4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUN-2000) to EMBL; U57551; AAB96359. INTERPRO; IPR000515; -. INTERPRO; IPR000719; -.
                                                       PFAM; PF00669; Flagellin_N; PFAM; PF00700; Flagellin_C; PRINTS; PR00207; FLAGELLIN. SEQUENCE 595 AA; 60937 MF
                                                                                                   Submitted (JUN-1999) to the EMBL; AB028471; BAA85080.1; INTERPRO; IPRO01029; -. INTERPRO; IPRO01492; -.
                                                                                                                                                                                   STRAIN-SU 1242;
                                                                                                                                                                                                                                            Escherichia coli.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                             FLAGELLIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A protective epitope of Moraxella catarrhalis different genes.";
                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                     NCBI_TaxID=562;
                                                                                                                                                                                                                                  Escherichia
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ch 10.5%; similarity 25.1%; 50; Conservative 3
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54; Conservative
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                                                                                                                                                            Ishioka K., Matsuba T., Ha
H antigen genes in E.coli
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                                                        MW;
                                                                                                                                                                                                                                            gamma subdivision;
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Score 98; DB Pred. No. 3.7; 30; Mismatches
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Pred. No. 4.8;
84; Mismatches
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Best Local S
Matches 52
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Q9KH34;
01-OCT-2000
01-OCT-2000
01-OCT-2000
         Can
                                     Q28243 PRELIMINARY; PRT; Q28243; Q28243; Q1-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1999 (TREMBLREL. 01, Last seg 01-NOV-1999 (TREMBLREL. 12, Last ann FIBRINGGEN A-ALPHA-CHAIN (FRAGMENT).
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"A metalloproteinase from antarctic bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF272770; AAF78076.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-643
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52; Conservative
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Proteobacteria; gam
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25.7%;
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METALLOPROTEINASE.
; 2DE912B5CA4CF73E CRC64;
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Best Local S
Matches 36
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01-JUN-1998
01-JUN-1998
01-JUN-2000
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                                                                                                                                Redenbach M., Kieser H.M.,
                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                               Submitted
                                                                                                                                                                                                                                                                    Parkhill J.,
                                                                                                                                                                                                                                                                                       STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                             Murphy L., Submitted
                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Actinomycetales;
NCBI_TaxID=1902;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                  microbiol. 21:77-96
; aL009199; CAA15789
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                                                                                                                                                                                                                                                                                                                                                           , Harris D.;
(DEC-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DEC-1994)
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MEDLINE=93269219; PubMed=8497848; Murakawa M., Okamura T., Kamura T., Shibuya T., Harada M., Niho Y.; Murakawa M., Okamura T., Kamura T., Shibuya T., Harada M., Niho Y.; "Diversity of primary structures of the carboxy-terminal regions of mammalian fibrinogen A alpha-chains. Characterization of the partial nucleotide and deduced amino acid sequences in five mammalian species."
                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacte
Actinomycetales; Streptomycineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thesus monkey, pig, dog, mouse and Thromb. Haemost. 69:351-360(1993). EMBL; D43756; BAA07813.1; -. HSSP; P02671; 1FZA.
the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21:77-96(1996).
                                       "A set of ordered cosmids and a
                                                                                                  STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
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                                                                                                                                                                                  B.G., F
to the
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24.5%; Pred. No.
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                                                                                                                                                                                  Rajandream M.A.;
e EMBL/GenBank/DDBJ
                                                                               Denapaite
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Last sequence up
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                                         detailed genetic and
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Query length: 183
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gb_est79:C05809
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AF122254 AF122254 Strongylocen
AL219461 Tetraodon nigrovirid
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 919 541-4899
Fax: 919 541-4571
Email: black009@niehs.nih.gov
Clone is available through Research Genetics,
Parkway, Huntsville, AL 35901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The NIEHS Xenopus Maternal EST Project Unpublished (2000)
Contact: Perry J. Blackshear
Office of Clinical Research and Laboratory National Institute of Environmental Health A2-05 NIEHS, 101 Alexander Drive, Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blackshear, P.J., Lai, W.S., Thorn, J.M., Kennington, E.A., St
Jr., Moore, D.T., Bouffard, G.G., Beckstrom-Sternberg, S.M.,
J.W., Bonaldo, M.F. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW632946.1 GI:7390026
EST.
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Seq primer: -21M13 forward primer (ABI).
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BACKWARD: CAGGAAACAGCTATGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  African clawed frog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR PRimers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phone 800-533-4363 ext.cdna, fax 256-536-9016 att:cdna, email
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             /note="vector: pT7T3-Pac; Site_1: EcoRI; Site_2: NotI; PolyA-selected mRNA was prepared from unfertilized Xenopus laevis eggs. The library was constructed in the vector pT7T3-Pac as described in Bonaldo, M.F., Lennon, G. and Soares, M.B. 'Normalization and subtraction: two approaches to facilitate gene discovery', Genome Research 6:791-806, 1996. The first strand synthesis used a NotI-dT18 primer; double stranded cDNAs were ligated to EcoRI adapters, digested with NotI, and directionally cloned into the NotI and EcoRI-digested pT7T3-Pac vector. The library contained approximately 7.2 x 10-5 recombinants, with average insert sizes of 1-1.5 kb."
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/clone_lib="Blackshear/Soares normalized Xenopus egg
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/db_xref="taxon:8355"
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Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
                                                                                                                                                                                                                                                                 AF122254 546 bp mRNA EST 18-OCT-1999 AF122254 Strongylocentrotus purpuratus early cleavage stage en Strongylocentrotus purpuratus cDNA clone 9_C06, mRNA sequence.
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Ratio:
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      Development 126 (17),
                                        EST analysis of gene expression in early cleavage-stage sea urchin
                                                                                                                    Strongylocentrotidae; Strongylocentrotus
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                                                              (bases 1 to 546)
;Y.H., Huang,G.M., Cameron,R.A., Graham,G.,
and Britten,R.J.
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LOCUS CNS02YBW
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131 TCAGCACCTGCCAGGACATCAAGAATCAAACATGGTTGGCCAGGACAAA 480
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AL219461.1
                                                    Tetraodon nigroviridis genome survey sequence T7 180G10 of library G from Tetraodon nigroviridis,
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Division of Biology
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/clone_lib="Strongylocentrotus purpuratus early cleavage
stage embryo"
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/db_xref="taxon:7668"
/clone="9_C06"
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                                                                                                                       308 AGCAGCAACAACCCCAGAGACAACAGCTGCAGCTACATCTGGTCCGACAA
95 hrAlaLeuGlyTrpThrValAlaTrpLys......
                                                                                                                                                                                                                                                                                                                                                     62 AlaLeuThrGlyThrTyrGluSerAlaValGlyAsnAlaGluSerArgTy
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                                                                                                                                                                                                 rValLeuThrGlyArgTyrAspSerAlaProAlaThrAspGlySerGlyT
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Roest-Crollius, H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottler,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using
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/clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Walbot V
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                                                                                                                                                                                                                                                                                                                                                                                                    Email: walbot@stanford.edu
Plate: 606061 row: B col
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                                             95.50
1.085
49.718
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                                                                                                Unpublished (1995)
Contact: Jun Takeda
Institute for Molecular and Cellular Regulation,
3-39-15 Showa-machi, Maebashi Gunma 371, Japan
Tel: 272-20-8856
Fax: 272-20-8896
                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 506)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to reverse of: AI770339 from: 1
                                                        jtakeda@sb.gunma-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ...GGCCAGGCGTCGTCAAGGTACTGGAGGATAATGACGG
                                       1. .506
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               506 bp
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                                                                                                                                                          Gunma University
                                                                                                                                                                                                                                                                                                    Euteleostomi;
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SOURCE
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                                                                                                                                                                                                                                                 seq_name:
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US-09-589-870-2 x C05809
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Quality:
                                                                        KEYWORDS
                                                                                                                    ACCESSION
                                                                                                                                                               DEFINITION
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                                                                                                                                                                                                                                                                                              460 CAGCTGG
                                                                                                                                                                                                                                                                                                                                     114 rThrTrp 116
                                                                                                                                                                                                                                                                                                                                                                                  410 GTGTGGCCTGTGGCAACGACATCGCCCTCATCAAGCTCTCACGCAGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      313 TTGGGCGAGTACGAC...CGTGCTGTGAAGGAGGGCCCCGAGCAGGTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213 TGGAAGCTTCTACCACACGTGTGGCGGTAGCCTCATCGCCCCCGACTGGG 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 GCGGTCCCCTACAGCTGGCCCTGGCAGGTTTCCCTGCAGTATGAGAAAAG 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 ATGGCCCACCTTCCTCGCCCTTCCAGCCGCGTTGTCAATGGTGAGGAT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 leValThrAlaGlyAlaAspGlyAlaLeuThrGlyThrTyrGluSerAla 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87 laProAlaThrAspGly......SerGlyThrAlaLeu 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 ValGlyAsnAlaGluSerArgTyrValLeuThrGlyArgTyrAspSer.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 uGlySerThrPhe..... 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 GlyIleThrGlyThrTrp......TyrAsnGlnLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 erAlaAspProSerLysAspSerLysAlaGlnValSerAlaAlaGluAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 CGATCCTCCCGCCTCGGCCTCTCAAAGCACTAGGATTACAGCCTCAGGCT 112
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                                                                                                                                                                                                                                                                                                                                                                                                                         GlyTrpThrValAlaTrpLysAsnAsnTyrArgAsnAlaHisSerAlaTh 114
                                                                                                                                                                                                                                                 gb_est36:AV432953
                                                                      Porphyra yezoensis
Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae;
                                                  Porphyra yezoensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                              466
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/clone_lib="Numan pancreatic islet"
/clone_lib="Numan pancreatic islet"
/note="Vector: Lambda ZAPII; Site_1: Eco RI; Site_2: Xho
I; mRNA was prepared from normal adult human islets. cDNA
was directionally synthesized from the Xho I in the vector
to the EcoRI site. cDNA was size fractionated to remove
sequences <1000 bp in size."

a 169 c 142 g 110 t 1 others
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Gaps: 6
Percent Identity: 26.797
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ORGANISM

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BASE COUNT
ORIGIN
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US-09-589-870-2 x AV432953
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                                                                                                                                    291
                                                                                                                                                                                                                                                                                                                                               156 GGGTGAGGAGCGCCCGGTCCCCTTCCCCCGACACGATTGTTCCCAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 lnTrpLeuLeuThrSerGlyThrThrGluAlaAsnAlaTrpLysSerThr 147
                                                                                                                                                                                                                                                                       244 GCCAAGATTGCCGATGCTCCG...GAGGACTCTATCCCGGACACCCCTGT
148 LeuValGlyHisAspThrPheThrLysValLysProSerAlaAlaSerIl 164
                                                                                                                                                                                                                             98 lyTrpThrValAlaTrpLysAsnAsnTyrArgAsnAlaHisSerAlaThr 114
                                                                                                                                                                                                                                                                                                         82 GlyArgTyrAspSerAlaProAlaThrAspGly.SerGlyThrAlaLeuG
                                                                                                                                                                                                                                                                                                                                                                                 66 hrTyrGlu...SerAlaValGlyAsnAlaGluSerArgTyrValLeuThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 GlnValSerAlaAlaGluAlaGlyIleThrGlyThrTrpTyrAsnGlnLe 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGACGCGTCGTCGCTGCCTGTTGCGGTGGCGTGACTAGCGCGGCCG
                                        GC.....GGCGGCGGCGGCAGCAGCAGCAGCAGCAGCAGCAGCAGC
                                                                                                                                                                                        CGTGGACCATCACGTGCCGGCGCCCCTTCCGCCGCGTCCGG......
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                                                                                                                  ...TGGTCGTGGCAGCACCGGAGGCGGAGGCGAAGCCCGATGTGCCGGAC
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Generation of 10,154 expressed sequence tags from a leafy gametophyte of a marine red alga, Porphyra yezoensis DNA Res. 7, 223-227 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Erika Asamizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 534)
Nikaido, I., Asamizu, E., Nakajima, M., Nakamura, Y., Saga, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tabata, S
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0.844
60.870
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/strain="TU-1"
/db_xref="taxon:2788"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="PM022b09_r"
/clone_lib="Porphyra yezoensis TU-1"
/note="Vector: pBluescriptII SK-; Site_1:
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Gaps:
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12
27.717
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ACCESSION
VERSION
KEYWORDS
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COMMENT
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AUTHORS
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                              US-09-589-870-2 \times AW677938/rev
                                                                                                                                                                                                                                         Align seg 1/1 to reverse of: AW677938
                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
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361 CCTCGACCTCGACCTCCTTGGTCTCAGTCTCGGCAGGAACAGCTTCCGCC
                                                                                  411 CGCCTCTGCTTCGTTGGTCTCTGTCTCTGCCTCGGCCGGCTCAGCCACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
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                                                                                                                                                               458 TCTGCTTCCTTGACCTCC...TCCGTCTCTGCTGCCGGCGCGCGCCTCGGC
                                                                                                                                                                               10 AlaValSerLeuThrThrValSerIleThrAlaSerAlaSerAlaSerAlaAspPr
                                                                                                                    26 oSerLysAspSerLysAlaGlnValSerAlaAlaGluAlaGlyIleThrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCATCGGT...GACGTCGCCGTCCGCGTCGTCCCCCATGCGCGAGGCAC
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                                            lyThrTrpTyrAsnGlnLeuGlySerThrPheIleValThrAlaGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gb_est47:AW677938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The University of Georgia
Plant Sciences Building, Rm.
Tel: 706 542 1860
Fax: 706 542 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Sorghum.

1 (bases 1 to 476)
Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudmar
                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: JEN REV
High quality sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
Contact: Cordonnier-Pratt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /Clone_lib="Water-stressed ] (WSl)"
/note="Organ: Mix of 5-week old plants on days 7 & 8 after
water was withheld; Vector: Lambda Zap; Site_1: XhoI;
Site_2: EcoRI; The library was made from poly-A RNA in the
cloning vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."

141 c 173 g 60 t
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1.106
65.385
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/db_xref="taxon:4558"
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Water-stressed 1 (WS1) S
                                                                                                                                                                                                                                                                                                                                        Gaps: 7
Percent Identity: 31.538
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bicolor cDN/
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alignment_block:
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Percent Similarity:
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                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 706 542 1860
Fax: 706 542 1805
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1 (bases 1 to 477)
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High quality sequence stop:
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nt Sciences Building, Rm.
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BE355782/rev
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                                                                                                                                                                                             /clone_lib="Dark Grown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
/note="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was
made from poly-a RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
146 c 174 g 61 t
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LOCUS BE357728
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                                                                                                                                                                                                                                                                                                            The University of Georgia Plant Sciences Building, Rm Tel: 706 542 1805 Fax: 706 542 1805 Email: mmpratt@uga.edu
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DG1_22_C07.b1_A002 Dark
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      An EST database from Sorghum: 
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sorghum bicolor
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                                                                                                                                                                                                                       Seq primer: JEN REV
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                                                                                                                                                                                                   quality sequence stop:
/db_xref="taxon:4558"
/clone_lib="Dark Grown 1 (DG1)"
/clone_lib="Dark Grown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
                                                                                                                /organism="Sorghum bicolor"
                                                                                                                                                            Location/Qualifiers
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Grown 1 (DG1) Sorghum
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AUTHORS
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LOCUS BE357007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCGGAGCCTCCTCGACGGGCACGGCAGTCGGGACCTGGACCTCGGCGGT 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gb_est70:BE357007
The University of Georgia Plant Sciences Building, Rm. : Tel: 706 542 1860 Fax: 706 542 1805 Email: mmpratt@uga.edu Sequences have been trimmed to
                                                                                                                                                                                                                                                                                                                                                                                                    BE357007 493 bp
DG1_146_D05.b1_A002 1
                                                                                                                                                                                                        Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Sorghum.

1 (bases 1 to 493)

Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and Pratt
                                                                                                                 Contact: Cordonnier-Pratt MM Department of Botany
                                                                                                                                                    , L.H.
An EST database from Sorghum: dark-grown seedlings
Unpublished (2000)
                                                                                                                                                                                                                                                                                       Sorghum bicolor
                                                                                                                                                                                                                                                                                                           sorghum.
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 to exclude PolyA, vector and regions
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                                                                           2502, Athens, GA 30602-7271,
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sorghum.
Sorghum bicolor
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Sorghum.
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DG1_40_E08.b1_A002
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a 147 c 179 g 63 t
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/db_xref="taxon:4558"
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                            Spermatophyta;
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US-09-589-870-2 x BE359336/rev
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Percent Similarity:
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GGCCATTGGTGCA...GCTAGGGTG....
                                   rValGlyGlyAlaGluAlaArgIleAsnThrGlnTrpLeu 133
                                                                           ACCGGAGCCTCCTCGACGGGCACGGCAGTCGGGACCTGGACCTCGGCGGT
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The University of Georgia
Plant Sciences Building, Rm.
Tel: 706 542 1805
Fax: 706 542 1805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 511)
Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Cordonnier-Pratt
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/note="Organ: 5-day-old dark-grown seedlings; Vector:
/note="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site_1: XhOI; Site_2: ECORI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
a 154 c 186 g 64 t
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/db_xref="taxon:4558"
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seq_documentation_block: LOCUS BE361106
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GGCGGCCGGGCTCTTCGACAACCGGAGCAGAGGCCTCCTTCGTTGGGTG
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                                                                                    {\tt rArgTyrValLeuThrGlyArgTyrAspSerAlaProAlaThrAspGly.}
                                                                                                                                                                                                                                                                                AspGlyAlaLeuThrGlyThrTyrGluSerAlaValGlyAsnAlaGluSe 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lyThrTrpTyrAsnGlnLeuGlySerThrPheIleValThrAlaGlyAla 59
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The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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DG1_69_F08.b1_A002 Dark Grown
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Sequences have been trimmed to exclude PolyA, vector and regions
Sequences have duality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 706 542 1860
Fax: 706 542 1805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sorghum bicolor
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/db_xref="taxon:4558"
/db_xref="taxon:4558"
/clone_lib="Dark Grown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
/note="Organ: 5-day-old dark-grown seedlings; Vector: 1-day-old dark-grown seedlings; Vect
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                                                                                  AlaValSerLeuThrThrValSerIleThrAlaSerAlaSerAlaAspPr
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Botany
The University of Georgia
Plant Sciences Building, 1
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BE357620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
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Fax: 706 542 1805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Sorghum.

1 (bases 1 to 538)
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                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Dark Grown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
/note="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site_1: xhoI; Site_2: EcoRI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
a 161 c 203 g 65 t
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1.106
65.385
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VERSION
KEYWORDS
 alignment_scores:
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Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The University of Georgia
Plant Sciences Building,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE357934 558 1
DG1_23_D10.b1_A002
                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 706 542 1860 Fax: 706 542 1805
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                                                                                                                                                                                                                                                                                                                                                                                              Email: mmpratt@uga.edu
Sequences have been tr:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Botany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Cordonnier-Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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                                                                                                                  115
                                                                                                                                                                                                                                                                                                                   quality sequence stop:
                                                                                                                                               /Clone_lib-"Dark Grown 1 (DG1)"
/note-"Organ: 5-day-old dark-grown seedlings; Vector:
/note-"Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site_1: xhOI; Site_2: EcoRI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II
                                                                                                            Clones to be sequenced were prepared by mass excision.
   94.00
1.106
                                                                                                                                                                                                                          /organism="Sorghum bicolor"
/db_xref="taxon:4558"
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Percent Similarity:

65.385

Percent Identity: 31.538

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TITLE
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AUTHORS
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US-09-589-870-2 x BE357934/rev
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LOCUS BE436254
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                                                                    source
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                                                                                                                                                                                                Clemson University
100 Jordan Hall, C.
                                                                                                                                                                                                                                                                    Unpublished (2000)
Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                  Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E., Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M., Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley
                                                                                                                                                         Tel: 864 656 4366
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
                                                                                                                                                                                                                                             Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                           Generation of ESTs from tomato fruit tissue, breaker stage
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                                                                                                                                    dfrisch@CLEMSON.EDU
                                                                                                                sequence.
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
                                                                                      ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                           215 TATCGAGTGGCACTCCATCGGCGATCATCCGGCGGATCCGAGCTGGAATT
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                                                                                                                                                                                  AlaArgIleAsnThrGlnTrpLeuLeuThrSerGlyThrThrGluAlaAs 142
..GATACGGCATCGCTTGAT 425
                                    roSerAlaAlaSerIleAsp 165
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/clone_lib="tomato breaker fruit,
/tissue_type="pericarp"
/dev_stage="breaker"
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